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(54) Title: PROTEINS INVOLVED IN THE REGULATION OF ENERGY HOMEOSTASIS

(57) Abstract: The present invention discloses novel uses for energy homeostasis regulating proteins and polynucleotides encoding these in the diagnosis, study, prevention, and treatment of metabolic diseases and disorders.

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Proteins involved in the regulation of energy homeostasis

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Description

This invention relates to the use of CG7956, aralar1, how (held out wings), CG9373, cpo (couch potato), Jafrac1 (thioredoxin peroxidase 1), or CG14440 homologous proteins, to the use of polynucleotides encoding these, and to the use of effectors/modulators of the proteins and polynucleotides in the diagnosis, study, prevention, and treatment of obesity and/or diabetes and/or metabolic syndrome.

There are several metabolic diseases of human and animal metabolism, eg., obesity and severe weight loss, that relate to energy imbalance where caloric intake versus energy expenditure is imbalanced. Obesity is one of the most prevalent metabolic disorders in the world. It is still a poorly understood human disease that becomes as a major health problem more and more relevant for western society. Obesity is defined as a body weight more than 20% in excess of the ideal body weight, frequently resulting in a significant impairment of health. Obesity may be measured by body mass index, an indicator of adiposity or fatness. Further parameters for defining obesity are waist circumferences, skinfold thickness and bioimpedance (see, inter alia, Kopelman (1999), loc. cit.). Obesity is associated with an increased risk for cardiovascular disease, hypertension, diabetes, hyperlipidaemia and an increased mortality rate. Besides severe risks of illness, individuals suffering from obesity are often isolated socially.

Obesity is influenced by genetic, metabolic, biochemical, psychological, and behavioral factors, and can be caused by different reasons such as non-insulin dependent diabetes, increase in triglycerides, increase in carbohydrate bound energy and low energy expenditure. As such, it is a

- 2 -

- complex disorder that must be addressed on several fronts to achieve lasting positive clinical outcome. Since obesity is not to be considered as a single disorder but as a heterogeneous group of conditions with (potential) multiple causes, it is also characterized by elevated fasting plasma insulin and an exaggerated insulin response to oral glucose intake (Koltermann J., (1980) Clin. Invest 65, 1272-1284). A clear involvement of obesity in type 2 diabetes mellitus can be confirmed (Kopelman P.G., (2000) Nature 404, 635-643).
- Hyperlipidemia and elevation of free fatty acids correlate clearly with the metabolic syndrome, which is defined as the linkage between several diseases, including obesity and insulin resistance. This often occurs in the same patients and are major risk factors for development of type 2 diabetes and cardiovascular disease. It was suggested that the control of lipid levels and glucose levels is required to treat type 2 diabetes, heart disease, and other occurrences of metabolic syndrome (see, for example, Santomauro A. T. et al., (1999) Diabetes, 48(9):1836-1841 and McCook, 2002, JAMA 288:2709-2716).
- The molecular factors regulating food intake and body weight balance are incompletely understood. Even if several candidate genes have been described which are supposed to influence the homeostatic system(s) that regulate body mass/weight, like leptin or the peroxisome proliferator-activated receptor-gamma co-activator, the distinct molecular mechanisms and/or molecules influencing obesity or body weight/body mass regulations are not known. In addition, several single-gene mutations resulting in obesity have been described in mice, implicating genetic factors in the etiology of obesity (Friedman and Leibel, 1990, Cell 69: 217-220). In the ob mouse a single gene mutation (obese) results in profound obesity, which is accompanied by diabetes (Friedman et. al., 1991, Genomics 11: 1054-1062).

- 3 -

Therefore, the technical problem underlying the present invention was to provide for means and methods for modulating (pathological) metabolic conditions influencing body-weight regulation and/or energy homeostatic circuits. The solution to said technical problem is achieved by providing the
5 embodiments characterized in the claims. Accordingly, the present invention relates to novel functions of proteins and nucleic acids encoding these in body-weight regulation, energy homeostasis, metabolism, and obesity. The proteins disclosed herein and polynucleotides encoding these are thus suitable to investigate metabolic diseases and disorders. Further
10 new compositions are provided that are useful in diagnosis, treatment, and prognosis of metabolic diseases and disorders as described.

KIAA0966 encodes for a Synaptojanin-like protein, the Sac domain-containing inositol phosphatase (hSac2). Synaptic vesicles are
15 recycled with remarkable speed and precision in nerve terminals. A major recycling pathway involves clathrin-mediated endocytosis at endocytic zones located around sites of release. Different 'accessory' proteins linked to this pathway have been shown to alter the shape and composition of lipid membranes, to modify membrane-coat protein interactions, and to
20 influence actin polymerization. These include the GTPase dynamin, the lysophosphatidic acid acyl transferase endophilin, and the phosphoinositide phosphatase synaptojanin (Brodin L. et al., 2000, Curr Opin Neurobiol 10(3):312-320). Studies on the endocytosis of synaptic vesicles have shown the essential roles of endophilin and synaptojanin in vesicle
25 formation (see, Ringstad N. et al., 1999, Neuron 24(1):143-154). The recessive suppressor of secretory defect in yeast Golgi and yeast actin function belongs to this family (Luo W. and Chang A., 1997, J Cell Biol 138(4):731-746). This protein may be involved in the coordination of the activities of the secretory pathway and the actin cytoskeleton. Human
30 synaptojanin, which may be localised on coated endocytic intermediates in nerve terminals also belongs to this family (Haffner C. et al., 1997, FEBS Lett 419(2-3):175-180). Studies on the endocytosis of synaptic vesicles

- 4 -

have shown the essential roles of endophilin and synaptojanin in vesicle formation (see, Ringstad N. et al., 1999, Neuron 24(1):143-154).

5 The human Sac domain-containing inositol phosphatase (hSac2) is ubiquitously expressed, but especially abundant in the brain, heart, skeletal muscle, and kidney. hSac2 protein exhibits 5-phosphatase activity specific for phosphatidylinositol 4,5-bisphosphate and phosphatidylinositol 3,4,5-trisphosphate (Minagawa T. et al., (2001) J Biol Chem 276(25):22011-22015).

10 Energy transduction in mitochondria requires the transport of many specific metabolites across the inner membrane of this eukaryotic organelle. The mitochondrial carrier family (MCF) consists of at least thirty-seven proteins. (Kuan J. and Saier M.H., 1993, Crit Rev Biochem Mol Biol 28(3):209-233).

15 The mitochondrial aspartate/glutamate carrier catalyzes an important step in both the urea cycle and the aspartate/malate NADH shuttle. Citrin and aralar1 are homologous proteins belonging to the mitochondrial carrier family with EF-hand Ca^{2+} binding motifs in their N-terminal domains. Citrin and aralar1 are isoform Ca^{2+} stimulated aspartate/glutamate transporters in mitochondria (Palmieri L. et al., 2001, EMBO J 20(18):5060-9). Solute carrier family 25, member 13 (SLC25A13) encodes a calcium-binding mitochondrial carrier protein, designated citrin. Mutations in the SLC25A13 gene lead to adult-onset type II citrullinemia (Yasuda T. et al., 2000, Hum Genet 107(6):537-545).

25 The held out wings (how) Drosophila gene encodes a RNA-binding protein involved in the control of muscular and cardiac activity. The how protein is localized to the nucleus. how is highly related to the mouse quaking gene which plays a role at least in myelination and that could serve to link a signal transduction pathway to the control of mRNA metabolism (Zaffran S. et al., 1997, Development 124(10):2087-2098). Two isoforms of the Drosophila RNA binding protein, how, act in opposing directions to regulate

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- 5 -

tendon cell differentiation (Nabel-Rosen H. et al., 2002, Dev Cell 2002 Feb;2(2):183-193). The opposing activities of the How isoforms are manifested by differential rates of mRNA degradation of the target stripe mRNA. This mechanism is conserved, as the mammalian RNA binding
5 Quaking proteins may similarly affect the levels of Krox20, a regulator of Schwann cell maturation.

The mouse quaking (qk) gene is essential in both myelination and early embryogenesis. Its product, QKI, is an RNA-binding protein belonging to a
10 growing protein family called STAR (signal transduction and activator of RNA) (Wu J. et al., 1999, J Biol Chem 274(41):29202-29210). Quaking is essential for blood vessel development (Noveroske J.K. et al., 2002, Genesis 32(3):218-230).

15 The myelin basic protein (MBP) gene is expressed in oligodendrocytes and Schwann cells, and expression follows a tightly regulated developmental time course. Cell type- and developmental stage-specific expression of the MBP gene is regulated by a series of cis-acting elements located upstream of the transcription start site. Myelin gene expression factor-2 (Myef-2), a
20 protein isolated from mouse brain represses transcription of the MBP gene. Myef-2 mRNA is developmentally regulated in mouse brain; its peak expression occurs at postnatal day 7, prior to the onset of MBP expression (Haas S. et al., 1995, J Biol Chem 270(21):12503-12510).

25 MBP is a major component of the myelin sheath whose production is developmentally controlled during myelinogenesis. Programmed expression of the MBP gene is regulated at the level of transcription. The MB1 regulatory motif plays an important role in transcription of the MBP promoter. The MB1 element contains a binding site for the repressor
30 protein MyEF-2 (Myelin gene expression factor-2). MyEF-2 is involved in transcriptional regulation of the MBP gene during the course of brain

- 6 -

development (Muralidharan V. et al., 1997, J Cell Biochem 1997 Sep 15;66(4):524-31).

5 The *Drosophila melanogaster* gene couch potato (*cpo*, GadFly Accession Number CG18434) encodes a putative nuclear RNA binding protein. The protein is expressed in the *Drosophila* embryo (embryonic central nervous system, embryonic peripheral nervous system, embryonic/larval midgut, glial cell and other tissues) (Harvie et al., 1998, Genetics 149(1): 217-231). At least three protein isoforms (for example, Cpo 17, Cpo 61.1
10 and Cpo 61.2) and 49 recorded mutant alleles have been described. Mutations have been isolated which affect the larval ventral ganglion and are recessive lethal in *Drosophila*. Mutant *cpo* flies exhibit an abnormal and hypoactive behavior (Bellen et al., 1992, Genetics 131: 365-375, and Bellen et al., 1992, Genes Dev. 6: 2125-2136). This invention describes as
15 human homolog proteins to the *Drosophila cpo* encoded gene product the RNA-binding protein gene with multiple splicing and a hypothetical protein XP_091097. No further information is available for the human homolog proteins from the prior art.

20 Incomplete reduction of atmospheric oxygen generates potent oxidizing agents, including reactive oxygen species (ROS) and their toxic byproducts. Protection from ROS is mediated by nonenzymatic agents, enzymes, and low molecular weight reducing agents, such as thioredoxin. Under normal conditions, thioredoxin reductase reduces oxidized
25 thioredoxin in the presence of NADPH. Reduced thioredoxin serves as an electron donor for thioredoxin peroxidase (peroxiredoxin) which consequently reduces H_2O_2 to H_2O (Schallreuter K.U. and Wood J.M., 2001, J Photochem Photobiol B 64(2-3):179-184). Members of the peroxiredoxin family play an antioxidant protective role in various tissues
30 under nonpathologic conditions and during inflammatory processes. Antioxidants govern intracellular reduction-oxidation (redox) status, which plays a critical role in NF κ B (nuclear factor kappa-B) transcription factor

- 7 -

activation. Different antioxidants are selective for redox regulation of certain transcription factors. Peroxidases of the peroxiredoxin family reduce hydrogen peroxide H_2O_2 and alkyl hydroperoxides to water and alcohol with the use of reducing equivalents derived from thiol-containing donor molecules.

A family of highly conserved antioxidant enzymes, Peroxiredoxins (Prxs), has two major Prx subfamilies: one subfamily uses two conserved cysteines (2-Cys) and the other uses 1-Cys to scavenge reactive oxygen species (ROS). Four mammalian 2-Cys members (Prx I-IV) utilize thioredoxin as the electron donor for antioxidation. Prxs are capable of protecting cells from ROS insult and regulating the signal transduction pathways that utilize c-Abl, caspases, nuclear factor-kappaB (NF-kappaB) and activator protein-1 (AP-1) to influence cell growth and apoptosis. Prxs are also essential for red blood cell (RBC) differentiation and are capable of inhibiting human immunodeficiency virus (HIV) infection and organ transplant rejection (Butterfield L.H. et al., 1999, Antioxid Redox Signal 1(4):385-402). Distribution patterns indicate that Prxs are highly expressed in the tissues and cells at risk for diseases related to ROS toxicity, such as Alzheimer's and Parkinson's diseases and atherosclerosis. This correlation suggests that Prxs are protective against ROS toxicity, yet overwhelmed by oxidative stress in some cells (Butterfield L.H. et al., 1999, Antioxid Redox Signal 1(4):385-402). Prxs tend to form large aggregates at high concentrations, a feature that may interfere with their normal protective function or may even render them cytotoxic. Imbalance in the expression of subtypes can also potentially increase their susceptibility to oxidative stress. Therefor Prxs may play a role in the cellular dysfunction of ROS-related diseases ranging from atherosclerosis to cancer to neurodegenerative diseases.

The Drosophila gene with GadFly Accession Number CG14440 encodes for a protein which is most homologous to the human hypothetical protein

- 8 -

LOC55565 (GenBank Accession Number NP_060000.1 for the protein, NM_017530 for the cDNA). No functional data are available for these proteins in the prior art.

5 So far, it has not been described that a protein of the invention or a homologous protein is involved in the regulation of energy homeostasis and body-weight regulation and related disorders, and thus, no functions in metabolic diseases and other diseases as listed above have been discussed. In this invention we demonstrate that the correct gene dose of
10 a protein of the invention is essential for maintenance of energy homeostasis. A genetic screen was used to identify that mutation of a gene encoding a protein of the invention or a homologous gene causes changes in the metabolism, in particular related to obesity, which is reflected by a significant change of triglyceride content, the major energy
15 storage substance.

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular methodology, protocols, cell lines, vectors, and reagents described as
20 these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention that will be limited only by the appended claims. Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly
25 understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods, devices, and materials are now described. All publications mentioned herein are incorporated herein by
30 reference for the purpose of describing and disclosing the cell lines, vectors, and methodologies that are reported in the publications which might be used in connection with the invention. Nothing herein is to be

- 9 -

construed as an admission that the invention is not entitled to antedate such disclosure.

5 The present invention discloses that CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 homologous proteins (herein referred to as "proteins of the invention" or "a protein of the invention") are regulating the energy homeostasis and fat metabolism especially the metabolism and storage of triglycerides, and polynucleotides, which identify and encode the proteins disclosed in this invention. The invention also relates to vectors, host cells,
10 antibodies, and recombinant methods for producing the polypeptides and polynucleotides of the invention. The invention also relates to the use of these sequences in the diagnosis, study, prevention, and treatment of metabolic diseases and dysfunctions, including metabolic syndrome, obesity, or diabetes as well as related disorders such as eating disorder, cachexia, hypertension, coronary heart disease, hypercholesterolemia,
15 dyslipidemia, osteoarthritis, or gallstones.

GadFly Accession Number CG7956, aralar1 (GadFly Accession Number CG2139), how (GadFly Accession Number CG10293), GadFly Accession
20 Number CG9373, cpo (GadFly Accession Number CG31243 and CG18434), Jafrac1 (GadFly Accession Number CG1633), or GadFly Accession Number CG14440 homologous proteins and nucleic acid molecules coding therefore are obtainable from insect or vertebrate species, e.g. mammals or birds. Particularly preferred are homologous
25 nucleic acids, particularly nucleic acids encoding a human protein as described in TABLE 1.

The invention particularly relates to a nucleic acid molecule encoding a polypeptide contributing to regulating the energy homeostasis and the
30 metabolism of triglycerides, wherein said nucleic acid molecule comprises
(a) the nucleotide sequence of CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 or homologous nucleic acids, particularly

- 10 -

nucleic acids encoding a human protein as described in Table 1, and/or a sequence complementary thereto,

(b) a nucleotide sequence which hybridizes at 50°C in a solution containing 1 x SSC and 0.1% SDS to a sequence of (a),

5 (c) a sequence corresponding to the sequences of (a) or (b) within the degeneration of the genetic code,

(d) a sequence which encodes a polypeptide which is at least 85%, preferably at least 90%, more preferably at least 95%, more preferably at least 98% and up to 99,6% identical to the amino acid
10 sequences of CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 homologous protein, preferably of a human homologous protein as described in Table 1.

(e) a sequence which differs from the nucleic acid molecule of (a) to (d) by mutation and wherein said mutation causes an alteration,
15 deletion, duplication and/or premature stop in the encoded polypeptide or

(f) a partial sequence of any of the nucleotide sequences of (a) to (e) having a length of 15 bases, preferably 20 bases, more preferably 25 bases and most preferably at least 50 bases.

20

The invention is based on the finding that CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 and/or homologous proteins and the polynucleotides encoding these, are involved in the regulation of triglyceride storage and therefore energy homeostasis. The invention
25 describes the use of these compositions for the diagnosis, study, prevention, or treatment of metabolic diseases or dysfunctions, including metabolic syndrome, obesity, or diabetes, as well as related disorders such as eating disorder, cachexia, hypertension, coronary heart disease, hypercholesterolemia, dyslipidemia, osteoarthritis, or gallstones.

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Accordingly, the present invention relates to genes with novel functions in body-weight regulation, energy homeostasis, metabolism, and obesity,

- 11 -

functional fragments of said genes, polypeptides encoded by said genes or fragments thereof, and effectors/modulators thereof, e.g. antibodies, biologically active nucleic acids, such as antisense molecules, RNAi molecules or ribozymes, aptamers, peptides or low-molecular weight organic compounds recognizing said polynucleotides or polypeptides.

The ability to manipulate and screen the genomes of model organisms such as the fly *Drosophila melanogaster* provides a powerful tool to analyze biological and biochemical processes that have direct relevance to more complex vertebrate organisms due to significant evolutionary conservation of genes, cellular processes, and pathways (see, for example, Adams M. D. et al., (2000) *Science* 287: 2185-2195). Identification of novel gene functions in model organisms can directly contribute to the elucidation of correlative pathways in mammals (humans) and of methods of modulating them. A correlation between a pathology model (such as changes in triglyceride levels as indication for metabolic syndrome including obesity) and the modified expression of a fly gene can identify the association of the human ortholog with the particular human disease.

In one embodiment, a forward genetic screen is performed in fly displaying a mutant phenotype due to misexpression of a known gene (see, Johnston *Nat Rev Genet* 3: 176-188 (2002); Rorth P., (1996) *Proc Natl Acad Sci U S A* 93: 12418-12422). In this invention, we have used a genetic screen to identify mutations of the CG7956, *aralar1*, *how*, CG9373, *cpo*, *Jafrac1*, or CG14440 gene, or homologous genes that cause changes in the body weight, which are reflected by a significant change of triglyceride levels.

Obese people mainly show a significant increase in the content of triglycerides. Triglycerides are the most efficient storage for energy in cells. In order to isolate genes with a function in energy homeostasis, several thousand proprietary and publicly available EP-lines were tested for their triglyceride content after a prolonged feeding period (see Examples for

- 12 -

more detail). Lines with significantly changed triglyceride content were selected as positive candidates for further analysis. The increase or decrease of triglyceride content due to the loss of a gene function suggests gene activities in energy homeostasis in a dose dependent manner that controls the amount of energy stored as triglycerides.

In this invention, the content of triglycerides of a pool of flies with the same genotype was analyzed after prolonged feeding using a triglyceride assay. Male flies homozygous or heterozygous for the integration of vectors for *Drosophila* EP-lines were analyzed in assays measuring the triglyceride contents of these flies, illustrated in more detail in the Examples section. The results of the triglyceride content analysis are shown in Figures 1, 5, 9, 13, 17, 21, and 25, respectively.

Genomic DNA sequences were isolated that are localized adjacent to the EP or PX vector integration. Using those isolated genomic sequences public databases like Berkeley *Drosophila* Genome Project (GadFly; see also FlyBase (1999) Nucleic Acids Research 27:85-88) were screened thereby identifying the integration sites of the vectors, and the corresponding genes, described in more detail in the Examples section. The molecular organization of the genes is shown in Figures 2, 6, 10, 14, 18, 22, and 26, respectively.

An additional screen using *Drosophila* mutants with modifications of the eye phenotype identified an interaction of *cpo* with *adipose*, a protein regulating, causing or contributing to obesity. An additional screen using *Drosophila* mutants with modifications of the eye phenotype identified a modification of UCP activity by *cpo*, thereby leading to an altered mitochondrial activity. These findings suggest the presence of similar activities of these described homologous proteins in humans that provides insight into diagnosis, treatment, and prognosis of metabolic disorders.

- 13 -

The *Drosophila* genes and proteins encoded thereby with functions in the regulation of triglyceride metabolism were further analysed in publicly available sequence databases (see Examples for more detail) and mammalian homologs were identified.

5

The function of the mammalian homologs in energy homeostasis was further validated in this invention by analyzing the expression of the transcripts in different tissues and by analyzing the role in adipocyte differentiation. Expression profiling studies (see Examples for more detail)

10 confirm the particular relevance of the protein(s) of the invention as regulators of energy metabolism in mammals. Further, we show that the proteins of the invention are regulated by fasting and by genetically induced obesity. In this invention, we used mouse models of insulin resistance and/or diabetes, such as mice carrying gene knockouts in the

15 leptin pathway (for example, ob (leptin) or db (leptin receptor) mice) to study the expression of the protein of the invention. Such mice develop typical symptoms of diabetes, show hepatic lipid accumulation and frequently have increased plasma lipid levels (see Bruning et al, 1998, Mol. Cell. 2:449-569).

20

Microarrays are analytical tools routinely used in bioanalysis. A microarray has molecules distributed over, and stably associated with, the surface of a solid support. The term "microarray" refers to an arrangement of a plurality of polynucleotides, polypeptides, antibodies, or other chemical

25 compounds on a substrate. Microarrays of polypeptides, polynucleotides, and/or antibodies have been developed and find use in a variety of applications, such as monitoring gene expression, drug discovery, gene sequencing, gene mapping, bacterial identification, and combinatorial chemistry. One area in particular in which microarrays find use is in gene

30 expression analysis (see Example 6). Array technology can be used to explore the expression of a single polymorphic gene or the expression profile of a large number of related or unrelated genes. When the

- 14 -

expression of a single gene is examined, arrays are employed to detect the expression of a specific gene or its variants. When an expression profile is examined, arrays provide a platform for identifying genes that are tissue specific, are affected by a substance being tested in a toxicology assay, are part of a signaling cascade, carry out housekeeping functions, or are specifically related to a particular genetic predisposition, condition, disease, or disorder.

Microarrays may be prepared, used, and analyzed using methods known in the art (see for example, Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796- Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:21502155; Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662). Various types of microarrays are well known and thoroughly described in Schena, M., ed. (1999; DNA Microarrays: A Practical Approach, Oxford University Press, London).

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotides described herein may be used as elements on a microarray. The microarray can be used in transcript imaging techniques, which monitor the relative expression levels of large numbers of genes simultaneously as described below. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor progression/regression of disease as a function of gene expression, and to develop and monitor the activities of therapeutic agents in the treatment of disease. In particular, this information may be used to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment regimen for that patient. For example, therapeutic agents, which are highly

- 15 -

effective and display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

As determined by Microarray analysis, Quaking 6 (QKI6), RNA binding
5 protein HQK-7B, RNA binding protein with multiple splicing (RBPMS),
Peroxisredoxin 1 (PRDX1), and hypothetical protein LOC55565 show
differential expression in human primary adipocytes. Thus, Quaking 6
(QKI6), RNA binding protein HQK-7B, RNA binding protein with multiple
splicing (RBPMS), Peroxisredoxin 1 (PRDX1), and hypothetical protein
10 LOC55565 are strong candidates for the manufacture of a pharmaceutical
composition and a medicament for the treatment of conditions related to
human metabolism, such as obesity, diabetes, and/or metabolic syndrome.

The invention also encompasses polynucleotides that encode a protein of
15 the invention or a homologous protein. Accordingly, any nucleic acid
sequence, which encodes the amino acid sequences of a protein of the
invention or a homologous protein, can be used to generate recombinant
molecules that express a protein of the invention or a homologous protein.
In a particular embodiment, the invention encompasses nucleic acids
20 encoding Drosophila CG7956, aralar1, how, CG9373, cpo, Jafrac1, or
CG14440 or human CG7956, aralar1, how, CG9373, cpo, Jafrac1, or
CG14440 homologs; referred to herein as the proteins of the invention. It
will be appreciated by those skilled in the art that as a result of the
degeneracy of the genetic code, a multitude of nucleotide sequences
25 encoding the proteins, some bearing minimal homology to the nucleotide
sequences of any known and naturally occurring gene, may be produced.
Thus, the invention contemplates each and every possible variation of
nucleotide sequence that could be made by selecting combinations based
on possible codon choices.

30

Also encompassed by the invention are polynucleotide sequences that are
capable of hybridizing to the claimed nucleotide sequences, and in

- 16 -

particular, those of the polynucleotides encoding CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440, or a homologous protein, preferably a human homologous protein as described in Table 1, under various conditions of stringency. Hybridization conditions are based on the melting
5 temperature (T_m) of the nucleic acid binding complex or probe, as taught in Wahl, G. M. and S. L. Berger (1987; Methods Enzymol. 152:399-407) and Kimmel, A. R. (1987; Methods Enzymol. 152:507-511), and may be used at a defined stringency. Preferably, hybridization under stringent conditions means that after washing for 1 h with 1 x SSC and 0.1% SDS
10 at 50°C, preferably at 55°C, more preferably at 62°C and most preferably at 68°C, particularly for 1 h in 0.2 x SSC and 0.1% SDS at 50°C, preferably at 55°C, more preferably at 62°C and most preferably at 68°C, a positive hybridization signal is observed. Altered nucleic acid sequences encoding the proteins which are encompassed by the invention include
15 deletions, insertions, or substitutions of different nucleotides resulting in a polynucleotide that encodes the same or a functionally equivalent protein.

The encoded proteins may also contain deletions, insertions, or substitutions of amino acid residues, which produce a silent change and
20 result in functionally equivalent proteins. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues as long as the biological activity of the protein is retained. Furthermore, the invention relates to peptide fragments of the proteins or
25 derivatives of such fragments such as cyclic peptides, retro-inverso peptides or peptide mimetics, wherein the peptides or derivatives usually have a length of at least four, preferably at least six and up to 50 amino acids.

30 Also included within the scope of the present invention are alleles of the genes encoding a protein of the invention or a homologous protein. As used herein, an "allele" or "allelic sequence" is an alternative form of the

- 17 -

gene, which may result from at least one mutation in the nucleic acid sequence. Alleles may result in altered mRNAs or polypeptides whose structures or function may or may not be altered. Any given gene may have none, one, or many allelic forms. Common mutational changes, which
5 give rise to alleles, are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

10 The nucleic acid sequences encoding a protein of the invention or a homologous protein may be extended utilizing a partial nucleotide sequence and employing various methods known in the art to detect upstream sequences such as promoters and regulatory elements. For example, one method which may be employed, "restriction-site" PCR, uses universal
15 primers to retrieve unknown sequence adjacent to a known locus (Sarkar, G. (1993) PCR Methods Applic. 2:318-322). Inverse PCR may also be used to amplify or extend sequences using divergent primers based on a known region (Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186). Another method which may be used is capture PCR which involves PCR
20 amplification of DNA fragments adjacent to a known sequence in human and yeast artificial chromosome DNA (Lagerstrom, M. et al. (PCR Methods Applic. 1:111-119). Another method which may be used to retrieve unknown sequences is that of Parker, J. D. et al. (1991; Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers, and
25 PROMOTERFINDER libraries to walk in genomic DNA (Clontech, Palo Alto, Calif.). This process avoids the need to screen libraries and is useful in finding intron/exon junctions.

In order to express a biologically active protein, the nucleotide sequences
30 encoding the proteins, may be inserted into appropriate expression vectors, i.e., a vector, which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods, which are well

- 18 -

- known to those skilled in the art, may be used to construct expression vectors containing sequences encoding the proteins and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. Such techniques are described in Sambrook, J. et al. (1989) *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. et al. (1989) *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, N.Y.
- 10 In a further embodiment of the invention, nucleic acid sequences encoding the sequences of the invention may be ligated to a heterologous sequence to encode a fusion protein. Heterologous sequences are preferably located at the N-and/or C-terminus of the fusion protein.
- 15 A variety of expression vector/host systems may be utilized to contain and express sequences encoding the proteins. These include, but are not limited to, micro-organisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (e.g., baculovirus); plant cell systems transformed with virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or PBR322 plasmids); or animal, e.g. mammalian cell systems.
- 20
- 25 The presence of polynucleotide sequences encoding a protein of the invention or a homologous protein can be detected by DNA-DNA or DNA-RNA hybridization or amplification using probes or portions or fragments of polynucleotides encoding a protein of the invention or a homologous protein. Nucleic acid amplification based assays involve the use of oligonucleotides or oligomers based on the sequences specific for the gene to detect transformants containing DNA or RNA encoding the corresponding protein. As used herein "oligonucleotides" or "oligomers"
- 30

- 19 -

refer to a nucleic acid sequence of at least about 10 nucleotides and as many as about 60 nucleotides, preferably about 15 to 30 nucleotides, and more preferably about 20-25 nucleotides, which can be used as a probe, primer or amplimer.

5

A variety of protocols for detecting and measuring the expression of proteins, using either polyclonal or monoclonal antibodies specific for the protein are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence
10 activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on the protein is preferred, but a competitive binding assay may be employed. These and other assays are described, among other places, in Hampton, R. et al. (1990; Serological Methods, a Laboratory Manual, APS Press, St
15 Paul, Minn.) and Maddox, D. E. et al. (1983; J. Exp. Med. 158:1211-1216).

20

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and proteins, e.g.
immunological assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding a protein of the invention or a homologous protein include oligo-labeling, nick translation, end-labeling of RNA probes or PCR amplification using a labeled
25 nucleotide. These procedures may be conducted using a variety of commercially available kits (Pharmacia & Upjohn, (Kalamazoo, Mich.); Promega (Madison Wis.); and U.S. Biochemical Corp., (Cleveland, Ohio).

30

Suitable reporter molecules or labels, which may be used for nucleic acid and protein assays, include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, co-factors, inhibitors, magnetic particles, and the like.

- 20 -

Host cells transformed with nucleotide sequences encoding the protein may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode the protein may be designed to contain signal sequences, which direct secretion of the protein through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding the protein to nucleotide sequence encoding a polypeptide domain, which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAG extension/affinity purification system (Immunex Corp., Seattle, Wash.) The inclusion of cleavable linker sequences such as those specific for Factor XA or Enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and the desired protein may be used to facilitate purification.

20

Diagnostics and Therapeutics

The data disclosed in this invention show that the nucleic acids and proteins of the invention and effectors/modulators thereof are useful in diagnostic and therapeutic applications implicated, for example but not limited to, in metabolic diseases or dysfunctions, including metabolic syndrome, obesity, or diabetes, as well as related disorders such as eating disorder, cachexia, hypertension, coronary heart disease, hypercholesterolemia, dyslipidemia, osteoarthritis, or gallstones. Hence, diagnostic and therapeutic uses for the nucleic acids and proteins of the invention are, for example but not limited to, the following: (i) protein

- 21 -

therapy, (ii) small molecule drug target, (iii) antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) diagnostic and/or prognostic marker, (v) gene therapy (gene delivery/gene ablation), (vi) research tools, and (vii) tissue regeneration in vitro and in vivo
5 (regeneration for all these tissues and cell types composing these tissues and cell types derived from these tissues).

The nucleic acids and proteins of the invention are useful in diagnostic and therapeutic applications implicated in various applications as described
10 below. For example, but not limited to, cDNAs encoding the proteins of the invention and particularly their human homologues may be useful in gene therapy, and the proteins of the invention and particularly their human homologues may be useful when administered to a subject in need thereof. By way of non-limiting example, the compositions of the present invention
15 will have efficacy for treatment of patients suffering from, for example, but not limited to, in metabolic disorders as described above.

The nucleic acid sequence encoding a protein of the invention, or a homologous protein, or a functional fragments thereof, may further be
20 useful in diagnostic applications, wherein the presence or amount of the nucleic acids or the proteins are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

25 For example, in one aspect, antibodies which are specific for a protein of the invention or a homologous protein may be used directly as an antagonist, or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express the protein. The
30 antibodies may be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimerical, single chain, Fab fragments, and fragments

- 22 -

produced by a Fab expression library. Neutralising antibodies, (i.e., those which inhibit dimer formation) are especially preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits,
5 rats, mice, humans, and others, may be immunized by injection with the protein or any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. It is preferred that the peptides, fragments, or oligopeptides used to induce antibodies to the protein have
10 an amino acid sequence consisting of at least five amino acids, and more preferably at least 10 amino acids.

Monoclonal antibodies to the proteins may be prepared using any technique that provides for the production of antibody molecules by
15 continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique (Köhler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R. J. et al. Proc. Natl. Acad. Sci. 80:2026-2030; Cole, S. P. et al. (1984) Mol. Cell
20 Biol. 62:109-120).

In addition, techniques developed for the production of "chimeric antibodies", the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and
25 biological activity can be used (Morrison, S. L. et al. (1984) Proc. Natl. Acad. Sci. 81:6851-6855; Neuberger, M. S. et al (1984) Nature 312:604-608; Takeda, S. et al. (1985) Nature 314:452-454). Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce
30 single chain antibodies specific for a protein of the invention or a homologous protein. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random

- 23 -

combinatorial immunoglobulin libraries (Burton, D. R. (1991) Proc. Natl. Acad. Sci. 88:11120-3). Antibodies may also be produced by inducing in vivo production in the lymphocyte population or by screening recombinant immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature (Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. 86:3833-3837; Winter, G. et al. (1991) Nature 349:293-299).

Antibody fragments which contain specific binding sites for the proteins may also be generated. For example, such fragments include, but are not limited to, the $F(ab')_2$ fragments which can be produced by Pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of $F(ab')_2$ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity (Huse, W. D. et al. (1989) Science 254:1275-1281).

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding and immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between the protein and its specific antibody. A two-site, monoclonal-based immunoassay utilising monoclonal antibodies reactive to two non-interfering protein epitopes are preferred, but a competitive binding assay may also be employed (Maddox, supra).

In another embodiment of the invention, the polynucleotides or fragments thereof, or nucleic acid effector molecules such as antisense molecules, aptamers, RNAi molecules or ribozymes may be used for therapeutic purposes. In one aspect, aptamers, i.e. nucleic acid molecules, which are capable of binding to a protein of the invention and modulating its activity

- 24 -

may be generated by a screening and selection procedure involving the use of combinatorial nucleic acid libraries.

In a further aspect, antisense molecules may be used in situations in which it would be desirable to block the transcription of the mRNA. In particular, 5 cells may be transformed with sequences complementary to polynucleotides encoding a protein of the invention or a homologous protein. Thus, antisense molecules may be used to modulate/effect protein activity, or to achieve regulation of gene function. Such technology is now 10 well known in the art, and sense or antisense oligomers or larger fragments, can be designed from various locations along the coding or control regions of sequences encoding the proteins. Expression vectors derived from retroviruses, adenovirus, herpes or vaccinia viruses, or from various bacterial plasmids may be used for delivery of nucleotide sequences to the 15 targeted organ, tissue or cell population. Methods, which are well known to those skilled in the art, can be used to construct recombinant vectors, which will express antisense molecules complementary to the polynucleotides of the genes encoding a protein of the invention or a homologous protein. These techniques are described both in Sambrook et 20 al. (supra) and in Ausubel et al. (supra). Genes encoding a protein of the invention or a homologous protein can be turned off by transforming a cell or tissue with expression vectors which express high levels of polynucleotide which encodes a protein of the invention or a homologous protein or a functional fragment thereof. Such constructs may be used to 25 introduce untranslatable sense or antisense sequences into a cell. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a month or more with a non-replicating vector and even longer if appropriate replication elements are part of the 30 vector system.

- 25 -

As mentioned above, modifications of gene expression can be obtained by designing antisense molecules, e.g. DNA, RNA, or nucleic acid analogues such as PNA, to the control regions of the genes encoding a protein of the invention or a homologous protein, i.e., the promoters, enhancers, and introns. Oligonucleotides derived from the transcription initiation site, e.g.,
5 between positions -10 and + 10 from the start site, are preferred. Similarly, inhibition can be achieved using "triple helix" base-pairing methodology. Triple helix pairing is useful because it cause inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances
10 using triplex DNA have been described in the literature (Gee, J. E. et al. (1994) In; Huber, B. E. and B. I. Carr, Molecular and Immunologic Approaches, Futura Publishing Co., Mt. Kisco, N.Y.). The antisense molecules may also be designed to block translation of mRNA by
15 preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary
20 target RNA, followed by endonucleolytic cleavage. Examples, which may be used, include engineered hammerhead motif ribozyme molecules that can be specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding a protein of the invention or a homologous protein. Specific ribozyme cleavage sites within any potential RNA target are
25 initially identified by scanning the target molecule for ribozyme cleavage sites which include the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides corresponding to the region of the target gene containing the cleavage site may be evaluated for secondary structural features which may render the
30 oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

- 26 -

Nucleic acid effector molecules, e.g. antisense molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding a protein of the invention or a homologous protein. Such DNA sequences may be incorporated into a variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize antisense RNA constitutively or inducibly can be introduced into cell lines, cells, or tissues. RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of non-traditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection and by liposome injections may be achieved using methods, which are well known in the art. Any of the therapeutic methods described above may be applied to any suitable subject including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

- 27 -

An additional embodiment of the invention relates to the administration of a pharmaceutical composition, in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic effects discussed above. Such pharmaceutical compositions may consist of a protein of the invention or a homologous nucleic acid sequence or protein, antibodies to a protein of the invention or a homologous protein, mimetics, agonists, antagonists, or inhibitors of a protein of the invention or a homologous protein or nucleic acid sequence. The compositions may be administered alone or in combination with at least one other agent, such as stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier, including, but not limited to, saline, buffered saline, dextrose, and water. The compositions may be administered to a patient alone, or in combination with other agents, drugs or hormones. The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries, which facilitate processing of the active compounds into preparations which, can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing Co., Easton, Pa.).

The pharmaceutical compositions of the present invention may be manufactured in a manner that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes. The pharmaceutical composition may be provided as a salt and can be formed

- 28 -

with many acids. After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of proteins, such labeling would include amount, frequency, and method of administration.

5

Pharmaceutical compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art. For any compounds, the therapeutically effective dose can be estimated initially
10 either in cell culture assays, e.g., of preadipocyte cell lines, or in animal models, usually mice, rabbits, dogs, or pigs. The animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans. A therapeutically effective
15 dose refers to that amount of active ingredient, for example a protein of the invention or a homologous protein or nucleic acid sequence or functional fragment thereof, or antibodies, which is sufficient for treating a specific condition. Therapeutic efficacy and toxicity may be determined
20 by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., ED50 (the dose therapeutically effective in 50% of the population) and LD50 (the dose lethal to 50% of the population). The dose ratio between therapeutic and toxic effects is the therapeutic index, and it can be expressed as the ratio, LD50/ED50. Pharmaceutical compositions,
25 which exhibit large therapeutic indices, are preferred. The data obtained from cell culture assays and animal studies is used in formulating a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage varies within this range
30 depending upon the dosage from employed, sensitivity of the patient, and the route of administration. The exact dosage will be determined by the practitioner, in light of factors related to the subject that requires

- 29 -

treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors, which may be taken into account, include the severity of the disease state, general health of the subject, age, weight, and gender of the subject, diet, time and frequency of administration, drug combination(s), reaction sensitivities, and tolerance/response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or once every two weeks depending on half-life and clearance rate of the particular formulation. Normal dosage amounts may vary from 0.1 to 100,000 micrograms, up to a total dose of about 1 g, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

In another embodiment, antibodies which specifically bind to a protein of the invention may be used for the diagnosis of conditions or diseases characterized by or associated with over- or underexpression of a protein of the invention or a homologous protein, or in assays to monitor patients being treated with a protein of the invention or a homologous protein, agonists, antagonists or inhibitors. The antibodies useful for diagnostic purposes may be prepared in the same manner as those described above for therapeutics. Diagnostic assays include methods which utilize the antibody and a label to detect the protein in human body fluids or extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by joining them, either covalently or non-covalently, with a reporter molecule. A wide variety of reporter molecules which are known in the art may be used several of which are described above.

- 30 -

A variety of protocols including ELISA, RIA, and FACS for measuring proteins are known in the art and provide a basis for diagnosing altered or abnormal levels of gene expression. Normal or standard values for gene expression are established by combining body fluids or cell extracts taken
5 from normal mammalian subjects, preferably human, with antibodies to the protein under conditions suitable for complex formation. The amount of standard complex formation may be quantified by various methods, but preferably by photometric means. Quantities of protein expressed in control and disease, samples e.g. from biopsied tissues are compared with the
10 standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides specific for a protein of the invention or a homologous protein may be used for
15 diagnostic purposes. The polynucleotides, which may be used, include oligonucleotide sequences, antisense RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantitate gene expression in biopsied tissues in which gene expression may be correlated with disease. The diagnostic assay may be used to distinguish between
20 absence, presence, and excess gene expression, and to monitor regulation of protein levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences,
25 encoding a protein of the invention or a homologous protein or closely related molecules, may be used to identify nucleic acid sequences which encode the respective protein. The hybridization probes of the subject invention may be DNA or RNA and are preferably derived from the nucleotide sequence of the polynucleotide encoding a CG7956, aralar1,
30 how, CG9373, cpo, Jafrac1, or CG14440 homologous protein, preferably a human homologous protein as described in Table 1 or from a genomic sequence including promoter, enhancer elements, and introns of the

- 31 -

naturally occurring gene. Means for producing specific hybridization probes for DNAs encoding a protein of the invention or a homologous protein include the cloning of nucleic acid sequences specific for a protein of the invention or a homologous protein into vectors for the production of mRNA probes. Such vectors are known in the art, commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, radionuclides such as ^{32}P or ^{35}S , or enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences specific for a protein of the invention or homologous nucleic acids may be used for the diagnosis of conditions or diseases, which are associated with the expression of the proteins. Examples of such conditions or diseases include, but are not limited to, metabolic diseases and disorders, including obesity and diabetes. Polynucleotide sequences specific for a protein of the invention or a homologous protein may also be used to monitor the progress of patients receiving treatment for metabolic diseases and disorders, including obesity and diabetes. The polynucleotide sequences may be used in Southern or Northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; or in dip stick, pin, ELISA or chip assays utilizing fluids or tissues from patient biopsies to detect altered gene expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences specific for a protein of the invention or homologous nucleic acids may be useful in assays that detect activation or induction of various metabolic diseases or dysfunctions, including metabolic syndrome, obesity, or diabetes. The nucleotide sequences may be labeled by standard methods, and added to a fluid or tissue sample from a patient under conditions suitable for the formation of

- 32 -

hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantitated and compared with a standard value. The presence of the associated disease. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or in monitoring the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disease associated with expression of a protein of the invention or a homologous protein, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, which is specific for nucleic acids encoding a protein of the invention or homologous nucleic acids, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with those from an experiment where a known amount of a substantially purified polynucleotide is used. Standard values obtained from normal samples may be compared with values obtained from samples from patients who are symptomatic for disease. Deviation between standard and subject values is used to establish the presence of disease. Once disease is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to evaluate whether the level of expression in the patient begins to approximate that, which is observed in the normal patient. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to metabolic diseases or dysfunctions, including metabolic syndrome, obesity, or diabetes, the presence of a relatively high amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more

- 33 -

definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the metabolic diseases and disorders. Additional diagnostic uses for oligonucleotides designed from the sequences encoding a protein of the invention or a homologous protein may involve the use of PCR. Such oligomers may be chemically synthesized, generated enzymatically, or produced from a recombinant source. Oligomers will preferably consist of two nucleotide sequences, one with sense orientation (5prime.fwdarw.3prime) and another with antisense (3prime.rarw.5prime), employed under optimized conditions for identification of a specific gene or condition. The same two oligomers, nested sets of oligomers, or even a degenerate pool of oligomers may be employed under less stringent conditions for detection and/or quantification of closely related DNA or RNA sequences.

Methods which may also be used to quantitate the expression of a protein of the invention or a homologous protein include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and standard curves onto which the experimental results are interpolated (Melby, P. C. et al. (1993) J. Immunol. Methods, 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 212:229-236). The speed of quantification of multiple samples may be accelerated by running the assay in an ELISA format where the oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantification.

In another embodiment of the invention, the nucleic acid sequences which are specific for a protein of the invention or homologous nucleic acids may also be used to generate hybridization probes, which are useful for mapping the naturally occurring genomic sequence. The sequences may be mapped to a particular chromosome or to a specific region of the chromosome using well known techniques. Such techniques include FISH, FACS, or artificial chromosome constructions, such as yeast artificial

- 34 -

chromosomes, bacterial artificial chromosomes, bacterial P1 constructions or single chromosome cDNA libraries as reviewed in Price, C. M. (1993) Blood Rev. 7:127-134, and Trask, B. J. (1991) Trends Genet. 7:149-154. FISH (as described in Verma et al. (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York, N.Y.) may be correlated with other physical chromosome mapping techniques and genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of the gene encoding a protein of the invention or a homologous protein on a physical chromosomal map and a specific disease, or predisposition to a specific disease, may help to delimit the region of DNA associated with that genetic disease.

The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier, or affected individuals. An analysis of polymorphisms, e.g. single nucleotide polymorphisms may be carried out. Further, in situ hybridization of chromosomal preparations and physical mapping techniques such as linkage analysis using established chromosomal markers may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of a particular human chromosome is not known. New sequences can be assigned to chromosomal arms, or parts thereof, by physical mapping. This provides valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the disease or syndrome has been crudely localized by genetic linkage to a particular genomic region, for example, AT to 11q22-23 (Gatti, R. A. et al. (1988) Nature 336:577-580), any sequences mapping to that area may represent associated or regulatory genes for further investigation. The nucleotide sequences of the subject invention may also be used to detect differences

- 35 -

in the chromosomal location due to translocation, inversion, etc. among normal, carrier, or affected individuals.

In another embodiment of the invention, a protein of the invention or a
5 homologous protein, its catalytic or immunogenic fragments or
oligopeptides thereof, an in vitro model, a genetically altered cell or animal,
can be used for screening libraries of compounds, e.g. peptides or
low-molecular weight organic compounds, in any of a variety of drug
screening techniques. One can identify modulators/effectors, e.g.
10 receptors, enzymes, proteins, ligands, or substrates that bind to, modulate
or mimic the action of one or more of the proteins of the invention. The
protein or fragment employed in such screening may be free in solution,
affixed to a solid support, borne on a cell surface, or located intracellularly.
The formation of binding complexes, between a protein of the invention or
15 a homologous protein and the agent tested, may be measured. Agents may
also, either directly or indirectly, influence the activity of the proteins of
the invention.

In addition activity of the proteins of the invention against their
20 physiological substrate(s) or derivatives thereof could be measured in
cell-based assays. Agents may also interfere with posttranslational
modifications of the proteins of the invention, such as phosphorylation and
dephosphorylation, farnesylation, palmitoylation, acetylation, alkylation,
ubiquitination, proteolytic processing, subcellular localization and
25 degradation. Moreover, agents could influence the dimerization or
oligomerization of the proteins of the invention or, in a heterologous
manner, of the proteins of the invention with other proteins, for example,
but not exclusively, docking proteins, enzymes, receptors, ion channels,
uncoupling proteins, or translation factors. Agents could also act on the
30 physical interaction of the proteins of this invention with other proteins,
which are required for protein function, for example, but not exclusively,
their downstream signaling.

- 36 -

The phosphatase activity of the Sac domain-containing inositol phosphatase 2 (SAC2) of the invention could be measured *in vitro* by using recombinantly expressed and purified SAC2 or fragments thereof by making use of artificial phosphatase substrates well known in the art, i.e. but not exclusively DiFMUP or FDP (Molecular Probes, Eugene, Oregon), which are converted to fluorophores or chromophores upon dephosphorylation. Alternatively, the dephosphorylation of physiological substrates of SAC2 could be measured by making use of any of the well known screening technologies suitable for the detection of the phosphorylation status of SAC2 inositol substrates, i.e. in a procedure similar as described for the inositol phosphatase SHIP2 (T. Habib et al. (1998), JBC 273, 18605-18609). In addition activity of SAC2 against its physiological substrate(s) or derivatives thereof could be measured in cell-based assays, thereby determining activity of the phosphatase at the level of their downstream signalling.

Methods for determining protein-protein interaction are well known in the art. For example binding of a fluorescently labeled peptide derived from a protein of the invention to the interacting protein (or vice versa) could be detected by a change in polarisation. In case that both binding partners, which can be either the full length proteins as well as one binding partner as the full length protein and the other just represented as a peptide are fluorescently labeled, binding could be detected by fluorescence energy transfer (FRET) from one fluorophore to the other. In addition, a variety of commercially available assay principles suitable for detection of protein-protein interaction are well known in the art, for example but not exclusively AlphaScreen (PerkinElmer) or Scintillation Proximity Assays (SPA) by Amersham. Alternatively, the interaction of the proteins of the invention with cellular proteins could be the basis for a cell-based screening assay, in which both proteins are fluorescently labeled and interaction of both proteins is detected by analysing cotranslocation of both proteins with a cellular imaging reader, as has been developed for example, but not

- 37 -

exclusively, by Cellomics or EvotecOAI. In all cases the two or more binding partners can be different proteins with one being the protein of the invention, or in case of dimerization and/or oligomerization the protein of the invention itself. Proteins of the invention, for which one target
5 mechanism of interest, but not the only one, would be such protein/protein interactions are CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 homologous proteins.

Assays for determining enzymatic and carrier activity of the proteins of the
10 invention are well known in the art. Well known in the art are also a variety of assay formats to measure receptor-ligand binding.

Of particular interest are screening assays for agents that have a low toxicity for mammalian cells. The term "agent" as used herein describes
15 any molecule, e.g. protein or pharmaceutical, with the capability of altering or mimicking the physiological function of one or more of the proteins of the invention. Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than
20 about 2,500 Daltons. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise carbocyclic or heterocyclic structures
25 and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups.

Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, nucleic acids and
30 derivatives, structural analogs or combinations thereof. Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for

- 38 -

random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides and oligopeptides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily
5 produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means, and may be used to produce combinatorial libraries. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification,
10 amidification, etc. to produce structural analogs. Where the screening assay is a binding assay, one or more of the molecules may be joined to a label, where the label can directly or indirectly provide a detectable signal.

Another technique for drug screening, which may be used, provides for
15 high throughput screening of compounds having suitable binding affinity to the protein of interest as described in published PCT application WO84/03564. In this method, as applied to a protein of the invention or a homologous protein, large numbers of different small test compounds are synthesized on a solid substrate, such as plastic pins or some other
20 surface. The test compounds are reacted with the proteins, or fragments thereof, and washed. Bound proteins are then detected by methods well known in the art. Purified proteins can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and
25 immobilize it on a solid support. In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding a protein of the invention specifically compete with a test compound for binding the protein. In this manner, the antibodies can be used to detect the presence of any peptide, which shares one or more
30 antigenic determinants with the protein of the invention.

- 39 -

The nucleic acids encoding the proteins of the invention can be used to generate transgenic cell lines and animals. These transgenic non-human animals are useful in the study of the function and regulation of the proteins of the invention in vivo. Transgenic animals, particularly
5 mammalian transgenic animals, can serve as a model system for the investigation of many developmental and cellular processes common to humans. A variety of non-human models of metabolic disorders can be used to test modulators of the protein of the invention. Misexpression (for example, overexpression or lack of expression) of the protein of the
10 invention, particular feeding conditions, and/or administration of biologically active compounds can create models of metabolic disorders.

In one embodiment of the invention, such assays use mouse models of insulin resistance and/or diabetes, such as mice carrying gene knockouts in
15 the leptin pathway (for example, ob (leptin) or db (leptin receptor) mice). Such mice develop typical symptoms of diabetes, show hepatic lipid accumulation and frequently have increased plasma lipid levels (see Bruning et al, 1998, Mol. Cell. 2:449-569). Susceptible wild type mice (for example C57Bl/6) show similar symptoms if fed a high fat diet. In addition
20 to testing the expression of the proteins of the invention in such mouse strains (see EXAMPLES section), these mice could be used to test whether administration of a candidate modulator alters for example lipid accumulation in the liver, in plasma, or adipose tissues using standard assays well known in the art, such as FPLC, colorimetric assays, blood
25 glucose level tests, insulin tolerance tests and others.

Transgenic animals may be made through homologous recombination in non-human embryonic stem cells, where the normal locus of the gene encoding the protein of the invention is mutated. Alternatively, a nucleic
30 acid construct encoding the protein is injected into oocytes and is randomly integrated into the genome. One may also express the genes of the invention or variants thereof in tissues where they are not normally

- 40 -

expressed or at abnormal times of development. Furthermore, variants of the genes of the invention like specific constructs expressing anti-sense molecules or expression of dominant negative mutations, which will block or alter the expression of the proteins of the invention may be randomly
5 integrated into the genome. A detectable marker, such as lac Z or luciferase may be introduced into the locus of the genes of the invention, where upregulation of expression of the genes of the invention will result in an easily detectable change in phenotype. Vectors for stable integration include plasmids, retroviruses and other animal viruses, yeast artificial
10 chromosomes (YACs), and the like.

DNA constructs for homologous recombination will contain at least portions of the genes of the invention with the desired genetic modification, and will include regions of homology to the target locus.
15 Conveniently, markers for positive and negative selection are included. DNA constructs for random integration do not need to contain regions of homology to mediate recombination. DNA constructs for random integration will consist of the nucleic acids encoding the proteins of the invention, a regulatory element (promoter), an intron and a poly-adenylation
20 signal. Methods for generating cells having targeted gene modifications through homologous recombination are known in the field. For non-human embryonic stem (ES) cells, an ES cell line may be employed, or embryonic cells may be obtained freshly from a host, e.g. mouse, rat, guinea pig, etc. Such cells are grown on an appropriate fibroblast-feeder layer and are
25 grown in the presence of leukemia inhibiting factor (LIF).

When non-human ES or non-human embryonic cells or somatic pluripotent stem cells have been transformed, they may be used to produce transgenic animals. After transformation, the cells are plated onto a feeder layer in an
30 appropriate medium. Cells containing the construct may be selected by employing a selective medium. After sufficient time for colonies to grow, they are picked and analyzed for the occurrence of homologous

- 41 -

recombination or integration of the construct. Those colonies that are positive may then be used for embryo transfection and blastocyst injection. Blastocysts are obtained from 4 to 6 week old superovulated females. The ES cells are trypsinized, and the modified cells are injected into the
5 blastocoel of the blastocyst. After injection, the blastocysts are returned to each uterine horn of pseudopregnant females. Females are then allowed to go to term and the resulting offspring is screened for the construct. By providing for a different phenotype of the blastocyst and the genetically modified cells, chimeric progeny can be readily detected. The chimeric
10 animals are screened for the presence of the modified gene and males and females having the modification are mated to produce homozygous progeny. If the gene alterations cause lethality at some point in development, tissues or organs can be maintained as allogenic or congenic grafts or transplants, or in vitro culture. The transgenic animals may be any
15 non-human mammal, such as laboratory animal, domestic animals, etc. The transgenic animals may be used in functional studies, drug screening, etc.

Finally, the invention also relates to a kit comprising at least one of

- (a) a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440
20 homologous nucleic acid molecule or a functional fragment thereof;
- (b) a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 homologous amino acid molecule or a functional fragment or an isoform thereof;
- (c) a vector comprising the nucleic acid of (a);
- 25 (d) a host cell comprising the nucleic acid of (a) or the vector of (c);
- (e) a polypeptide encoded by the nucleic acid of (a);
- (f) a fusion polypeptide encoded by the nucleic acid of (a);
- (g) an antibody, an aptamer or another effector/modulator against the nucleic acid of (a) or the polypeptide of (b), (e), or (f) and
- 30 (h) an anti-sense oligonucleotide of the nucleic acid of (a).

- 42 -

The kit may be used for diagnostic or therapeutic purposes or for screening applications as described above. The kit may further contain user instructions.

5 The Figures show:

Figure 1 shows the triglyceride content of a *Drosophila* Gadfly Accession Number CG7956 mutant. Shown is the change of triglyceride content of HD-EP(3)31805 flies caused by integration of the P-vector 3 base pairs 5' of the CG7956 transcription unit (referred to as 'HD-EP31805', column 2)
10 in comparison to controls containing all flies of the EP collection (referred to as 'EP-control', column 1).

Figure 2 shows the molecular organization of the mutated CG7956 (*Gadfly* Accession Number) gene locus.
15

Figure 3 shows the BLASTP search result for the *Gadfly* Accession Number CG7956 gene product (Query) with the best human homologous match (Sbjct).
20

Figure 4 shows the expression of the CG7956 homolog in mammalian tissues.

Figure 4A shows the real-time PCR analysis of Sac domain-containing inositol phosphatase 2 (SAC2) expression in wild-type mouse tissues.

25 Figure 4B shows the real-time PCR analysis of SAC2 expression in different mouse models.

Figure 5 shows the triglyceride content of a *Drosophila* aralar 1 (*Gadfly* Accession Number CG2139) mutant. Shown is the change of triglyceride content of EP(3)3675 flies caused by integration of the P-vector into an intron of the CG2139 gene (referred to as 'EP(3)3675', column 2) in
30

- 43 -

comparison to controls containing all flies of the EP collection (referred to as 'EP-control', column 1).

5 Figure 6 shows the molecular organization of the mutated aralar 1 (Gadfly Accession Number CG2139) gene locus.

Figure 7 shows the homology of Drosophila aralar 1 to human solute carrier family 25, members 11 and 12.

10 Figure 7A shows the BLASTP search results for the aralar 1 gene product (Query) with the two best human homologous matches (Sbjct).

Figure 7B shows the comparison of human and Drosophila proteins. 'alarar1 Dm' refers to Drosophila protein encoded by aralar 1, 'SLC25A12 Hs' refers to human solute carrier family 25, member 12, and 'SLC25A13 Hs' refers to human solute carrier family 25, member 13.

15

Figure 8 shows the expression of the aralar 1 homologs in mammalian tissues.

Figure 8A shows the real-time PCR analysis of solute carrier family 25, member 12 (Slc25a12) expression in wild-type mouse tissues.

20 Figure 8B shows the real-time PCR analysis of Slc25a12 expression in different mouse models.

Figure 8C shows the real-time PCR analysis of solute carrier family 25, member 13 (Slc25a13) expression in wild-type mouse tissues.

25 Figure 8D shows the real-time PCR analysis of Slc25a13 expression in different mouse models.

30 Figure 9 shows the triglyceride content of a Drosophila how (Gadfly Accession Number CG10293) mutant. Shown is the change of triglyceride content of HD-EP(3)30815 flies caused by integration of the P-vector into the promoter of the how gene (referred to as 'HD-EP30815', column 2) in comparison to controls containing all flies of the EP collection (referred to as 'EP-control', column 1).

- 44 -

Figure 10 shows the molecular organization of the mutated how (Gadfly Accession Number CG10293) gene locus.

Figure 11 shows the homology of Drosophila how (GadFly Accession Number CG10293) to the human quaking isoforms.

Figure 11A shows the BLASTP search result for the how gene product (Query) with the twelve best human homologous matches (Sbjct).

Figure 11B shows the comparison of human and Drosophila proteins. 'CG10293 Dm' refers to Drosophila protein encoded by CG10293, 'QKI-6 Hs' refers to human QUAKING isoform 6, 'QKI-2 Hs' refers to human QUAKING isoform 2, 'QKI-3 Hs' refers to human QUAKING isoform 3, and 'HQB-7B Hs' refers to human RNA binding protein HQB-7B.

Figure 12 shows the expression of how homologs in mammalian (human) tissue.

Figure 12A shows the quantitative analysis of QUAKING 6 expression in human abdominal adipocyte cells, during the differentiation from preadipocytes to mature adipocytes.

Figure 12B shows the quantitative analysis of RNA binding protein HQB-7B expression in human abdominal adipocyte cells, during the differentiation from preadipocytes to mature adipocytes.

Figure 13 shows the triglyceride content of a Drosophila Gadfly Accession Number CG9373 mutant. Shown is the change of triglyceride content of HD-EP(3)31646 flies caused by ectopic expression of the CG9373 gene mainly in the neurons of these flies (referred to as 'HD-EP3646/elav', column 2) in comparison to controls with integration of this vector (referred to as 'random EP/elav', column 1).

Figure 14 shows the molecular organization of the mutated CG9373 (Gadfly Accession Number) gene locus.

- 45 -

Figure 15 shows the homology of *Drosophila* GadFly Accession Number CG9373 to human KIAA1443 protein, unnamed protein product, and myelin gene expression factor 2.

Figure 15A shows the BLASTP search result for the CG9373 gene product (Query) with the three best human homologous matches (Sbjct).

Figure 15B shows the comparison of human and *Drosophila* proteins. 'CG9373 Dm' refers to *Drosophila* protein encoded by CG9373, 'KIAA1341 Hs' refers to human KIAA1341 protein, 'MyEF-2 Hs' refers to human myelin gene expression factor 2, and 'FLJ13071 Hs' refers to human unnamed protein product FLJ13071.

Figure 16 shows the expression of the CG9373 homolog in mammalian tissues.

Figure 16A shows the real-time PCR analysis of myelin gene expression factor 2 (MEF-2) expression in wild-type mouse tissues.

Figure 16B shows the real-time PCR analysis of MEF-2 expression in different mouse models.

Figure 16C shows the real-time PCR analysis of MEF-2 expression in mice fed with a high fat diet compared to mice fed with a standard diet.

Figure 17 shows the triglyceride content of a *Drosophila* cpo (Gadfly Accession Number CG18434) mutant. Shown is the change of triglyceride content of EP(3)0661 flies caused by integration of the P-vector into the promoter of the CG18434 gene (referred to as 'EP(3)0661/Tm3,Sb' column 2) in comparison to controls containing all flies of the EP collection (referred to as 'EP-control', column 1).

Figure 18 shows the molecular organization of the mutated cpo (Gadfly Accession Number CG18434) gene locus.

Figure 19 shows the homology of *Drosophila* cpo to human RNA binding proteins with multiple splicing.

- 46 -

Figure 19A shows the comparison of human and Drosophila proteins. 'cpo Dm' refers to Drosophila protein encoded by cpo, 'NP_006858 Hs' refers to human RNA binding protein with multiple splicing (RBPMS), and 'IPI001611' refers to human RNA binding with multiple splicing (RBPMS) family member.

Figure 19B shows the amino acid sequence encoded by Drosophila cpo gene (GadFly Accession Number CG31243, SEQ ID NO:1).

Figure 20 shows the quantitative analysis of RNA binding protein with multiple splicing (RBPMS) expression in human abdominal adipocyte cells, during the differentiation from preadipocytes to mature adipocytes.

Figure 21 shows the triglyceride content of a Drosophila Jafrac1 (Gadfly Accession Number CG1633) mutant. Shown is the change of triglyceride content of PX9430.2 flies caused by integration of the P-vector into the leader of the Jafrac1 gene (referred to as 'PX 9430.2', column 2) in comparison to controls without integration of this vector, (herein referred to as 'PX-control', column 1).

Figure 22 shows the molecular organization of the mutated Jafrac1 (Gadfly Accession Number CG1633) gene locus.

Figure 23 shows the homology of Drosophila Jafrac1 (GadFly Accession Number CG1633) to human peroxiredoxin 1 and 2.

Figure 23A shows the BLASTP search result for the Jafrac1 gene product (Query) with the best two human homologous matches (Sbjct).

Figure 23B shows the comparison of human and Drosophila proteins. 'Jafrac1 Dm' refers to Drosophila protein encoded by Jafrac1, 'PRDX1 Hs' refers to human peroxiredoxin 1, and 'PRDX2 Hs' refers to human peroxiredoxin 2.

- 47 -

Figure 24 shows the quantitative analysis of peroxiredoxin 1 (PRDX1) expression in human abdominal adipocyte cells, during the differentiation from preadipocytes to mature adipocytes.

5 Figure 25 shows the triglyceride content of a Drosophila Gadfly Accession Number CG14440 mutant. Shown is the change of triglyceride content of PX10162.1 flies caused by integration of the P-vector upstream of the CG14440 gene (referred to as 'PX10162.1', column 2) in comparison to controls without integration of this vector, (herein referred to as
10 'PX-control', column 1).

Figure 26 shows the molecular organization of the mutated CG14440 (Gadfly Accession Number) gene locus.

15 Figure 27 shows the BLASTP search result for the CG14440 gene product (Query) with the best human homologous match (Sbjct).

Figure 28 shows the quantitative analysis of hypothetical protein LOC55565 expression in human abdominal adipocyte cells, during the
20 differentiation from preadipocytes to mature adipocytes.

The examples illustrate the invention:

25 Example 1: Measurement of triglyceride content in Drosophila

Mutant flies are obtained from proprietary and publicly available fly mutation stock collections. The flies are grown under standard conditions known to those skilled in the art. In the course of the experiment,
30 additional feedings with bakers yeast (*Saccharomyces cerevisiae*) are provided. The average change of triglyceride content of Drosophila containing the EP-vectors in homozygous or heterozygous viable

- 48 -

integration was investigated in comparison to control flies (see Figures 1, 5, 9, 13, and 17, 21, and 25). For determination of triglyceride, flies were incubated for 5 min at 90°C (in case of PX9430.2 and PX10162.1 at 70°C) in an aqueous buffer using a waterbath, followed by hot extraction.

5 After another 5 min incubation at 90°C (in case of PX9430.2 and PX10162.1 at 70°C) and mild centrifugation, the triglyceride content of the flies extract was determined using Sigma Triglyceride (INT 336-10 or -20) assay by measuring changes in the optical density according to the manufacturer's protocol. As a reference protein content of the same

10 extract was measured using BIO-RAD DC Protein Assay according to the manufacturer's protocol for the EP-lines. The assays were repeated several times.

The average triglyceride level of all flies of the EP collections (referred to as 'EP-control') is shown as 100% in the first columns in Figures 1, 5, 9, and 17, respectively. The average triglyceride level of about 50 lines of the PX collection (referred to as 'PX-control') is shown as 100% in the first column in Figures 21 and 25 (relative amount of triglyceride per fly). The average triglyceride level of all flies containing the elav- Gal4 vector

20 (referred to as 'random EP/elav') is shown as 100% in the first column in Figure 13. Standard deviations of the measurements are shown as thin bars.

HD-EP(3)31805 homozygous flies (column 2 in Figure 1), EP(3)0661

25 heterozygous flies (column 2 in Figure 17, referred to as 'EP(3)0661/TM3,Sb'), PX9430.2 homozygous flies (column 2 in Figure 21), and PX10162.1 homozygous flies (column 2 in Figure 25) show constantly a higher triglyceride content than the controls. EP(3)3675 homozygous flies (column 2 in Figure 5) and HD-EP(3)30815 homozygous

30 flies (column 2 in Figure 9) show constantly a lower triglyceride content than the controls. Therefore, the loss of gene activity in the loci where the

- 49 -

EP-vectors or PX-vectors are viably integrated, is responsible for changes in the metabolism of the energy storage triglycerides.

HD-EP(3)31646 males were crossed to elav-Gal4 virgins. The offspring
5 carries a copy of the HD-EP(3)31646 vector and a copy of the elav-Gal4
vector, leading to ectopic expression of adjacent genomic DNA sequences
3prime of the HD-EP(3)31646 integration locus, mainly in the neurons of
these flies. The flies were analyzed in an assay measuring the triglyceride
content of these flies. The result of the triglyceride content analysis is
10 shown in Figure 13. HD-EP(3)31646/elav flies show constantly a higher
triglyceride content (column 2 in Figure 13) than the control EP-collection
that is crossed to elav-Gal4 (referred to as 'random EP/elav', column 1 in
Figure 13). Therefore, the gain of gene activity in the locus, where the
EP-vector of HD-EP(3)31646 flies is integrated in the promoter of the
15 CG9373 gene, is responsible for changes in the metabolism of the energy
storage triglycerides.

Example 2: Identification of Drosophila genes associated with regulation of
20 metabolism

Nucleic acids encoding the proteins of the present invention were identified
using a plasmid-rescue technique. Genomic DNA sequences were isolated
that are localized adjacent to the EP vector (herein HD-EP(3)31805,
25 EP(3)3675, HD-EP(3)30815, HD-EP(3)31646, EP(3)0661, PX9430.2, or
PX10162.1) integration. Using those isolated genomic sequences public
databases like Berkeley Drosophila Genome Project (GadFly) were screened
thereby identifying the integration sites of the vectors, and the
corresponding genes. The molecular organization of these gene loci is
30 shown in Figures 2, 6, 10, 14, 18, 22, and 26.

- 50 -

In Figures 2, 10, 14, and 26, genomic DNA sequence is represented by the assembly as a dotted black line in the middle that includes the integration sites of the vectors for lines HD-EP(3)31805, HD-EP(3)30815, HD-EP(3)31646, or PX10162.1. Numbers represent the coordinates of the genomic DNA. The upper parts of the figures represent the sense strand " + ", the lower parts represent the antisense strand "-". The insertion sites of the P-elements in the Drosophila lines are shown as triangles or boxes in the "P-elements +", "P-elements -", or middle lines. Transcribed DNA sequences (ESTs) are shown as grey bars in the "EST +" and/or the "EST -" lines, and predicted cDNAs are shown as bars in the "cDNA +" and/or "cDNA -" lines. Predicted exons of the cDNAs are shown as dark grey bars and introns are shown as light grey bars.

In Figures 6, 18, and 22, genomic DNA sequence is represented by the assembly as a thin black scaled double-headed arrow in the middle that includes the integration sites of the vectors for lines EP(3)3675, EP(3)0661, or PX9430.2. Numbers and ticks represent the length of the genomic DNA (1000 base pairs per tick in Figure 6, 10000 base pairs per tick in Figures 18 and 22). The upper part of the figure represents the sense strand, the lower part represent the antisense strand. The grey arrows in the upper part of Figures 6 and 22, and the dark grey box in the topmost part of Figure 18 represent BAC clones, the black arrows in the topmost part of Figures 6 and 22, and the light grey box in the middle of Figure 18 represent the sections of the chromosomes or GenBank units. The insertion sites of the P-elements in the Drosophila lines are shown as grey triangles in Figures 6 and 18, and as black vertical line in Figure 22. The P-insertion sites are labeled. Grey bars, linked by black lines represent cDNA sequences. Predicted genes are shown as black bars (exons), linked by black lines (Figures 6 and 22) or light grey serrated lines (Figure 18) (introns), and are labeled (see also key at the bottom of the figures).

- 51 -

The HD-EP(3)31805 vector is homozygous viable integrated 3 base pairs 5' of a Drosophila gene in antisense orientation, identified as GadFly Accession Number CG7956. The chromosomal localization site of the integration of the vector of HD-EP(3)31805 is at gene locus 3R, 93E4. In Figure 2, the coordinates of the genomic DNA are starting at position 17260000 on chromosome 3R, ending at position 17270000. The insertion site of the P-element in Drosophila HD-EP(3)31805 line is shown in the "P Elements -" line and is labeled. The predicted cDNA of the CG7956 gene is shown in the "cDNA +" line and is labeled.

The EP(3)3675 vector is homozygous viable integrated into an intron of a Drosophila gene in sense orientation, identified as aralar1 (GadFly Accession Number CG2139). The chromosomal localization site of the integration of the vector of EP(3)3675 is at gene locus 3R, 99F6. In Figure 6, the insertion site of the P-element in Drosophila EP(3)3675 line is shown in the as triangle in the lower part of the figure and labeled with an arrow. The predicted transcription variants of the Drosophila aralar1 gene (GadFly Accession Number CG2139) are shown as black boxes, linked with thin black lines.

The HD-EP(3)30815 vector is homozygous viable integrated into the promoter of a Drosophila gene in antisense orientation, identified as how (GadFly Accession Number CG10293). The chromosomal localization site of the integration of the vector of HD-EP(3)30815 is at gene locus 3R, 94A1-2. In Figure 10, the coordinates of the genomic DNA are starting at position 17775577 on chromosome 3R, ending at position 17775577. The insertion site of the P-element in Drosophila HD-EP(3)30815 line is shown in the "P-elements -" line. The predicted cDNA of the how gene is shown in the "cDNA +" line and is labeled.

The HD-EP(3)31646 vector is homozygous viable integrated into the promoter region of a Drosophila gene in sense orientation, identified as

- 52 -

GadFly Accession Number CG9373. The chromosomal localization site of the integration of the vector of HD-EP(3)31646 is at gene locus 3R, 85D25. In Figure 14, the coordinates of the genomic DNA are starting at position 5312505 on chromosome 3R, ending at position 5318755. The
5 insertion site of the P-element in Drosophila HD-EP(3)31646 line is shown in the "P-elements -" line. The predicted cDNA of the CG9373 gene is shown in the "cDNA -" line and is labeled.

The EP(3)0661) vector is homozygous lethal / heterozygous viable
10 integrated into the promoter of RE30936.5 in sense orientation, representing an EST-clone of a Drosophila gene, identified as cpo (GadFly Accession Numbers CG18434 and CG31243). The chromosomal localization site of the integration of the vector of EP(3)0661 is at gene locus 3R, 90D1. In Figure 18, the insertion site of the P-element in
15 Drosophila EP(3)0661 line is shown as triangle in the upper part of the figure and labeled with an arrow. The predicted cDNA of the cpo gene is shown in the upper part of the figure and is labeled.

The PX9430.2 vector is homozygous viable integrated into the leader
20 sequence of a Drosophila gene, identified as Jafrac1 (GadFly Accession Number CG1633). The chromosomal localization site of the integration of the vector of PX9430.2 is at gene locus X, 11E6. In Figure 22, the insertion site of the P-element in Drosophila PX9430.2 line is shown as vertical labeled line. The predicted transcript variants of the Drosophila
25 Jafrac1 gene are shown in the upper part of the figure and are labeled.

The PX10162.1 vector is homozygous viable integrated upstream of the
5'-end of a Drosophila gene, identified as GadFly Accession Number CG14440. The chromosomal localization site of the integration of the
30 vector of PX10162.1 is at gene locus X, 6C7. In Figure 26, the coordinates of the genomic DNA are starting at position 6494082 on chromosome X, ending at position 6519082. The insertion site of the

- 53 -

P-element in *Drosophila* PX10162.1 line is shown as "+" on the dotted middle line. The predicted cDNA of CG14440 shown in the "cDNA -" line and is labeled, the corresponding EST is shown in the "EST -"line and is labeled.

5

Expression of the genes described above could be affected by integration of the vectors into the transcription units, leading to a change in the amount of the energy storage triglycerides.

10

Example 3: Identification of human homologous genes and proteins

The *Drosophila* genes and proteins encoded thereby with functions in the regulation of triglyceride metabolism were further analysed using the
15 BLAST algorithm searching in publicly available sequence databases and mammalian homologs were identified (see Table 1 and Figures 3, 7, 11, 15, 19, 23, and 27).

Table 1: Human homologs of the Drosophila (Dm) genes

Dm gene Acc. No. Name	Homo sapiens homologous genes and proteins		
	Accession Number		Name
	cDNA	Protein	
CG7956	NM_014937	NP_055752	Sac domain-containing inositol phosphatase 2 (SAC2); KIAA0966
CG2139 <i>aralar1</i>	NM_003705	NP_003696	solute carrier family 25 (mitochondrial carrier, Aralar), member 12 (SLC25A12)
	NM_014251	NP_055066	solute carrier family 25, member 13 (citrin) (SLC25A13)
CG10293 <i>how</i>	AF142419	AAF63414	QUAKING isoform 6 (QUAKING)
	AF142418	AAF63413	QUAKING isoform 2 (QUAKING)
	AF142422	AAF63417	QUAKING isoform 3 (QUAKING)
	AB067801	BAB69499	RNA binding protein HQK-7B
CG9373	AB037762	BAA92579	KIAA1341 protein
	AK023133	BAB14421	unnamed protein product FLJ13071
	NM_016132	NP_057216	myelin gene expression factor 2 (MEF-2)
CG31243 CG18434 <i>cpo</i>	NM_006867	NP_006858	RNA binding protein with multiple splicing (RBPMS)
	ENSG00000166831	ENSP00000300069	RNA binding with multiple splicing (RBPMS) family member
CG1633 <i>Jafrac1</i>	NM_002574	NP_002565	peroxiredoxin 1 (PRDX1)
	BC000452	AAH00452	protein similar to thioredoxin peroxidase 1
CG14440	NM_017530	NP_060000	hypothetical protein LOC55565 (LOC55565)

CG7956, *aralar1*, *how*, CG9373, *cpo*, *Jafrac1*, or CG14440 homologous proteins and nucleic acid molecules coding therefore are obtainable from insect or vertebrate species, e.g. mammals or birds. Particularly preferred are nucleic acids as described in Table 1.

The present invention is describing polypeptides comprising the amino acid sequences of the proteins of the invention. Comparisons (Clustal W 1.83

- 55 -

analysis, see for example Thompson J. D. et al., (1994) Nucleic Acids Res. 22(22):4673-4680; Thompson J. D., (1997) Nucleic Acids Res 25(24):4876-4882; Higgins, D. G. et al., (1996) Methods Enzymol. 266:383-402) between the respective proteins of different species (human
5 and Drosophila) were conducted. Gaps in the alignment are represented as -. Based upon homology, the Drosophila proteins of the invention and each homologous protein or peptide may share at least some activity.

As shown in Figure 3, gene product of Drosophila GadFly Accession
10 Number CG7956 is 52% homologous to human Sac domain-containing inositol phosphatase (SAC2, also referred to as KIAA0966 protein; GenBank Accession Number NP_055752.1 for the protein, NM_014937 for the cDNA). CG7956 also shows homology to mouse protein ENSMUSP00000045910 (ENSEMBL Accession Number).

15 Human solute carrier family 25 (mitochondrial carrier, Aralar), member 12 is also referred to as GenBank Accession Number XP_010876.3 for the protein, XM_010876 for the cDNA. As shown in Figure 7A, the gene product of Drosophila aralar 1 is 74% homologous to human solute carrier
20 family 25 (mitochondrial carrier, Aralar), member 12 and 73% homologous to human solute carrier family 25, member 13 (citrin). aralar 1 also shows homology to mouse solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 13 (GenBank Accession Number NP_056644.1).

25 As shown in Figure 11A, gene product of Drosophila how is 64% homologous to human QUAKING isoform 5 (GenBank Accession Number AAF63416.1 for the protein, AF142421 for the cDNA), 64% homologous to human protein similar to KH domain RNA binding protein QKI-5A
30 (GenBank Accession Number XP_037438.2 for the protein, XM_037438 for the cDNA), 64% homologous to QUAKING isoform 6 (GenBank Accession Number AAF63414.1 for the protein, AF142419 for the cDNA),

- 56 -

64% homologous to unnamed protein product (GenBank Accession Number BAB55032.1 for the protein, AK027309 for the cDNA), 67% homologous to QUAKING isoform 2 (GenBank Accession Number AAF63413.1 for the protein, AF142418 for the cDNA), 67% homologous to QUAKING isoform 3 (GenBank Accession Number AAF63417.1 for the protein, AF142422 for the cDNA), 67% homologous to QUAKING isoform 4 (GenBank Accession Number AAF63415.1 for the protein, AF142420 for the cDNA), 67% homologous to QUAKING isoform 3 (GenBank Accession Number AAF63417.1 for the protein, AF142422 for the cDNA), 67% homologous to RNA binding protein HQK-6 (GenBank Accession Number BAB69497.1 for the protein, AB067799 for the cDNA), 67% homologous to RNA binding protein HQK-7B (GenBank Accession Number BAB69499.1 for the protein, AB067801 for the cDNA), 67% homologous to RNA binding protein HQK-7 (GenBank Accession Number BAB69498.1 for the protein, AB067800 for the cDNA), 67% homologous to QUAKING isoform 1 (GenBank Accession Number AAF63412.1 for the protein, AF142417 for the cDNA), and 64% to genes related to stomach cancer (GenBank Accession Number BD004960.1. Drosophila how also shows homology to mouse KH domain RNA binding protein QKI-7B (GenBank Accession Number AAC63042.1).

As shown in Figure 15A, gene product of Drosophila GadFly Accession Number CG9373 is 44% homologous to human KIAA1341 protein (GenBank Accession Number BAA92579.1 for the protein, AB037762 for the cDNA), 43% homologous to human unnamed protein product (GenBank Accession Number BAB14421.1 for the protein, AK023133 for the cDNA), and 43% to myelin gene expression factor 2 (GenBank Accession Number NP_057216.1 for the protein, NM_016132 for the cDNA. CG9373 also shows homology to mouse myelin gene expression factor (GenBank Accession Number AAL90778.1).

- 57 -

Drosophila cpo is also referred to as SEQ ID NO:1 in Figure 19B. Human RNA-binding protein gene with multiple splicing (RBPMS) is also referred to as GenBank Accession Number XP_047075.1 for the protein, XM_047075 for the cDNA, and human gene similar to RNA-binding protein with multiple
5 splicing is also referred to as GenBank Accession Number XP_091097 for the protein, XM_091097 for the cDNA. As shown in Figure 19A, the gene product of Drosophila CG31243 is 62% homologous to human RNA-binding protein with multiple splicing and 59% homologous to human protein similar to RNA-binding protein with multiple splicing at the
10 C-terminal part, respectively.

As shown in Figure 23A, gene product of Drosophila Jafrac1 is 83% homologous to human peroxiredoxin 2 (GenBank Accession Number XP_009063.2 for the protein, XM_009062 for the cDNA) and 82%
15 homologous to human peroxiredoxin 1 (GenBank Accession Number NP_002565.1 for the protein, NM_002574 for the cDNA). CG1633 also shows homology to mouse thioredoxin dependent peroxide reductase 2 (GenBank Accession Number NP_035164.1) and to mouse peroxiredoxin 4 (GenBank Accession Number NP_048044.1).

20 As shown in Figure 27, gene product of Drosophila GadFly Accession Number CG14440 is 57% homologous to human hypothetical protein LOC55565 (GenBank Accession Number NP_060000.1 for the protein, NM_017530 for the cDNA). CG14440 also shows homology to mouse
25 protein similar to hypothetical protein LOC55565 (GenBank Accession Number AAH23180.1).

The human Jafrac1 homologous protein peroxiredoxin 1 is also referred to as natural killer cell enhancing factor A in Patent Number US5610286-A.
30 The human Jafrac1 homologous protein peroxiredoxin 2 is also referred to as amino acid sequence of the acid form of peroxyredoxin TDX1 in Patent Number FR2798672-A1. The human CG14440 homologous protein is also

- 58 -

referred to as human polypeptide SEQ ID NO 3381 in Patent Number WO200153312-A1.

5 Example 4: Genetic adipose pathway screen

Adipose (adp) is a protein that has been described as regulating, causing or contributing to obesity in an animal or human (see WO 01/96371). Transgenic flies containing a wild type copy of the adipose cDNA under the control of the Gal4/UAS system were generated (Brand and Perrimon, 10 1993, Development 118:401-415; for adipose cDNA, see WO 01/96371). Chromosomal recombination of these transgenic flies with an eyeless-Gal4 driver line has been used to generate a stable recombinant fly line over-expressing adipose in the developing Drosophila eye. Animals 15 receiving transgenic adipose activity under these conditions developed into adult flies with a visible change of eye phenotype. Virgins of the recombinant driver line were crossed with males of the mutant EP-line collection in single crosses and kept for preferably 12 to 15 days at 29°C. The offspring was checked for modifications of the eye phenotype 20 (enhancement or suppression). Mutations changing the eye phenotype affect genes that modify adipose activity. The inventors have found that the fly line HD-EP(3)35715 is a suppressor of the eye-adp-Gal4 induced eye phenotype. This result is strongly suggesting an interaction of the cpo gene with adipose since the integration of HD-EP(3)35715 was found to be 25 located at the cpo locus. This is supporting the function of cpo and homologous proteins in the regulation of the energy homeostasis.

Example 5: dUCPy modifier screen

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Expression of Drosophila uncoupling protein dUCPy in a non-vital organ like the eye (Gal4 under control of the eye-specific promoter of the "eyeless"

- 59 -

gene) results in flies with visibly damaged eyes. This easily visible eye phenotype is the basis of a genetic screen for gene products that can modify UCP activity.

5 Parts of the genomes of the strain with Gal4 expression in the eye and the strain carrying the pUAST-dUCPy construct were combined on one chromosome using genomic recombination. The resulting fly strain has eyes that are permanently damaged by dUCPy expression. Flies of this strain were crossed with flies of a large collection of mutagenized fly
10 strains. In this mutant collection a special expression system (EP-element, Ref.: Rorth P, Proc Natl Acad Sci U S A 1996, 93(22):12418-22) is integrated randomly in different genomic loci. The yeast transcription factor Gal4 can bind to the EP-element and activate the transcription of endogenous genes close the integration site of the EP-element. The
15 activation of the genes therefore occurs in the same cells (eye) that overexpress dUCPy. Since the mutant collection contains several thousand strains with different integration sites of the EP-element it is possible to test a large number of genes whether their expression interacts with dUCPy activity. In case a gene acts as an enhancer of UCP activity the eye
20 defect will be worsened; a suppressor will ameliorate the defect.

Using this screen a gene with suppressing activity was discovered that was found to be the cpo gene in Drosophila.

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Example 6: Expression of the polypeptides in mammalian (mouse) tissues

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For analyzing the expression of the polypeptides disclosed in this invention in mammalian tissues, several mouse strains (preferably mice strains C57Bl/6J, C57Bl/6 ob/ob and C57Bl/KS db/db which are standard model systems in obesity and diabetes research) were purchased from Harlan Winkelmann (33178 Borcheln, Germany) and maintained under constant

- 60 -

temperature (preferably 22°C), 40 per cent humidity and a light / dark cycle of preferably 14 / 10 hours. The mice were fed a standard chow (for example, from ssniff Spezialitäten GmbH, order number ssniff M-Z V1126-000). For the fasting experiment ("fasted wild type mice"), wild type mice were starved for 48 h without food, but only water supplied ad libitum (see, for example, Schnetzler et al., (1993) J Clin Invest 92(1):272-280, Mizuno et al., (1996) Proc Natl Acad Sci U S A 93(8):3434-3438). Animals were sacrificed at an age of 6 to 8 weeks. The animal tissues were isolated according to standard procedures known to those skilled in the art, snap frozen in liquid nitrogen and stored at -80°C until needed.

RNA was isolated from mouse tissues using Trizol Reagent (for example, from Invitrogen, Karlsruhe, Germany) and further purified with the RNeasy Kit (for example, from Qiagen, Germany) in combination with an DNase-treatment according to the instructions of the manufacturers and as known to those skilled in the art. Total RNA was reverse transcribed (preferably using Superscript II RNaseH- Reverse Transcriptase, from Invitrogen, Karlsruhe, Germany) and subjected to Taqman analysis preferably using the Taqman 2xPCR Master Mix (from Applied Biosystems, Weiterstadt, Germany; the Mix contains according to the Manufacturer for example AmpliTaq Gold DNA Polymerase, AmpErase UNG, dNTPs with dUTP, passive reference Rox and optimized buffer components) on a GeneAmp 5700 Sequence Detection System (from Applied Biosystems, Weiterstadt, Germany).

Taqman analysis was performed preferably using the following primer/probe pairs:

For the amplification of Sac domain-containing inositol phosphatase 2 (sac2) (SEQ ID NO: 1): 5'- CCT GGA TCG CAC CAA CG -3'; mouse sac2 reverse primer (SEQ ID NO: 2): 5'- TTA AGC TGC TGT TCC ATG ACC A

- 61 -

-3'; Taqman probe (SEQ ID NO: 3): (5/6-FAM) TCC AGG CTG CCA TAG CGC GC (5/6-TAMRA)

For the amplification of mouse solute carrier family 25 (mitochondrial carrier, Aralar) member 12 (Slc25a12) (SEQ ID NO: 4): 5'- CCT GCC AAC CCT GAT CAC A -3'; mouse Slc25a12 reverse primer (SEQ ID NO: 5): 5'- TTT CAA TGC CAG CGA AAG TG -3'; Taqman probe (SEQ ID NO: 6): (5/6-FAM) CGG TGG CTA CAG ACT TGC CAC GG (5/6-TAMRA)

For the amplification of mouse solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 13 (Slc25a13) (SEQ ID NO: 7): 5'- AGC GGT GGT TCT ATG TCG ATT T -3'; mouse Slc25a13 reverse primer (SEQ ID NO: 8): 5'- CGG GAT TTA GGA ACC GGC T -3'; Taqman probe (SEQ ID NO: 9): (5/6-FAM) AGG CGT GAA GCC CGT GGG ATC T (5/6-TAMRA)

For the amplification of mouse myelin gene expression factor 2 (mef2) (SEQ ID NO: 10): 5'- ACA AGG ATG GCA AGA GCA GAG -3'; mouse mef2 reverse primer (SEQ ID NO: 11): 5'- ATG GAA ATT GCT TGG ACT GCT T -3'; Taqman probe (SEQ ID NO: 12): (5/6-FAM) CAT GGG CAC TGT CAC TTT TGA GCA GG (5/6-TAMRA)

In the figures the relative RNA-expression is shown on the Y-axis. In Figures 4A and B, 8A, B, C, and D, and 16A, B, and C, the tissues tested are given on the X-axis. "WAT" refers to white adipose tissue, "BAT" refers to brown adipose tissue.

As shown in Figure 4A, real time PCR (Taqman) analysis of the expression of the Sac domain-containing inositol phosphatase 2 (SAC2) RNA in mammalian (mouse) tissues revealed that SAC2 is highly expressed in hypothalamus, brain, WAT, spleen and kidney. Figure 4B shows that SAC2 is upregulated in BAT and pancreas of fasted animals as well as ob / ob

- 62 -

mice. The arcuate nucleus in the hypothalamus is the region in the brain that regulates feeding behaviour. The high expression level of SAC2 in the hypothalamus and WAT strongly suggests that this gene plays a central role in energy homeostasis. This is supported by the upregulation of SAC2 in BAT and the pancreas of two animal models used to study metabolic disorders.

As shown in Figure 8A, real time PCR (Taqman) analysis of the expression of the solute carrier family 25, member 12 (Slc25a12) RNA in mammalian (mouse) tissues revealed that Slc25a12 is highly expressed in muscle, hypothalamus, brain and heart. As shown in Figure 8B, Slc25a12 is nine-fold upregulated in BAT of ob /ob mice and more than two-fold upregulated in BAT of fasted animals. Slc25a12 is nearly three-fold downregulated in the heart of ob /ob mice. As shown in Figure 8C, solute carrier family 25, member 13 (Slc25a13) is highly expressed in liver, heart and kidney of wild type animals. As shown in Figure 8D, Slc25a13 is strongly upregulated in BAT of ob /ob mice and more than four-fold downregulated in heart tissue of ob /ob mice. The tissue specific expression of Slc25a12 and Slc25a13 together with the clear regulation in BAT and heart in the genetic model for obesity, suggests that Slc25a12 and Slc25a13 play a central role in the metabolism.

As shown in Figure 16A, real time PCR (Taqman) analysis of the expression of the myelin gene expression factor 2 (MEF-2) RNA in mammalian (mouse) tissues revealed that MEF-2 is highly expressed in hypothalamus, brain and testis. Furthermore it shows robust expression levels in WAT, colon, lung, spleen and kidney. Figure 16B shows that MEF-2 is upregulated in BAT of ob / ob mice. Figure 16C shows that MEF-2 is also upregulated in BAT after high fat (palmitate) diet feeding. The upregulation of MEF-2 in BAT of a genetic model of obesity as well as under high fat diet suggests a central role for MEF-2 in metabolism.

- 63 -

Example 7. Analysis of the differential expression of transcripts of the proteins of the invention in human tissues

RNA preparation from human primary adipose tissues was done as described in Example 6. The hybridization and scanning was performed as described in the manufacturer's manual (see Affymetrix Technical Manual, 2002, obtained from Affmetrix, Santa Clara, USA).

In Figures 12A and B, 20, 24, and 28, the X-axis represents the time axis, shown are day 0 and day 12 of adipocyte differentiation. The Y-axis represents the fluorescent intensity. The expression analysis (using Affymetrix GeneChips) of the Quaking 6 (QKI6), RNA binding protein HQK-7B, RNA binding protein with multiple splicing (RBPMS), Peroxiredoxin 1 (PRDX1), and hypothetical protein LOC55565 genes using primary human abdominal adipocyte differentiation clearly shows differential expression of human QKI6, HQK-7B, RBPMS, PRDX1, and LOC55565 genes in adipocytes. Several independent experiments were done. The experiments show that the QKI6 (see Figure 12A), HQK-7B (see Figure 12B), and PRDX1 (see Figure 24) are most abundant at day 12 compared to day 0 during differentiation. The experiments further show that the RBPMS (see Figure 20) and LOC55565 (see Figure 28) transcripts are most abundant at day 0 compared to day 12 during differentiation.

Thus, the QKI6, HQK-7B, or PRDX1 proteins have to be significantly increased in order for the preadipocytes to differentiate into mature adipocyte. The QKI6, HQK-7B, or PRDX1 prroteins in preadipocytes have the potential to enhance adipose differentiation at a very early stage. The RBPMS or LOC55565 proteins have to be significantly decreased in order for the preadipocytes to differentiate into mature adipocyte. Therefore, the RBPMS or LOC55565 proteins in preadipocytes have the potential to inhibit adipose differentiation at a very early stage.

- 64 -

Therefore, QKI6, HQK-7B, RBPMS, PRDX1, and LOC55565 proteins might play an essential role in the regulation of human metabolism, in particular in the regulation of adipogenesis and thus it might play an essential role in obesity, diabetes, and/or metabolic syndrome.

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For the purpose of the present invention, it will understood by the person having average skill in the art that any combination of any feature mentioned throughout the specification is explicitly disclosed herewith.

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- 65 -

Claims

1. A pharmaceutical composition comprising a CG7956, aralar1, how,
5 CG9373, cpo, Jafrac1, or CG14440 nucleic acid molecule
or a polypeptide encoded thereby and/or a functional fragment
thereof or an effector/modulator of said nucleic acid molecule and/or
a polypeptide encoded thereby, preferably together with
pharmaceutically acceptable carriers, diluents and/or additives.
10
2. The composition of claim 1, wherein the nucleic acid molecule is a
vertebrate or insect CG7956, aralar1, how, CG9373, cpo, Jafrac1,
or CG14440 nucleic acid, particularly encoding a human protein as
described in Table 1, and/or a nucleic molecule which is
15 complementary thereto, or a functional fragment thereof or a variant
thereof.
3. The composition of claim 1 or 2, wherein said nucleic acid molecule
is selected from the group consisting of
20 (a) a nucleic acid molecule encoding a polypeptide as shown in
Table 1;
(b) a nucleic acid molecule which comprises or is the nucleic acid
molecule as shown in Table 1;
(c) a nucleic acid molecule degenerate as a result of the genetic
25 code to the nucleic acid sequences as defined (a) or (b);
(d) a nucleic acid molecule that hybridizes at 50°C in a solution
containing 1 x SSC and 0.1 % SDS to a nucleic acid molecule
as defined in claim 2 and/or a nucleic acid molecule which is
complementary thereto;
30 (e) a nucleic acid molecule that encodes a polypeptide which is
at least 85%, preferably at least 90%, more preferably at
least 95%, more preferably at least 98% and up to 99,6%

- 66 -

identical to a human protein as described in Table 1 or as defined in claim 2; and

- (f) a nucleic acid molecule that differs from the nucleic acid molecule of (a) to (e) by mutation and wherein said mutation causes an alteration, deletion, duplication or premature stop in the encoded polypeptide.

5

4. The composition of any one of claims 1-3, wherein the nucleic acid molecule is a DNA molecule, particularly a cDNA or a genomic DNA.

10

5. The composition of any one of claims 1-4, wherein said nucleic acid encodes a polypeptide contributing to regulating the energy homeostasis and/or the metabolism of triglycerides.

15

6. The composition of any one of claims 1-5, wherein said nucleic acid molecule is a recombinant nucleic acid molecule.

7. The composition of any one of claims 1-6, wherein the nucleic acid molecule is a vector, particularly an expression vector.

20

8. The composition of any one of claims 1-5, wherein the polypeptide is a recombinant polypeptide.

9. The composition of claim 8, wherein said recombinant polypeptide is a fusion polypeptide.

25

10. The composition of any one of claims 1-7, wherein said nucleic acid molecule is selected from hybridization probes, primers and anti-sense oligonucleotides.

30

11. The composition of any one of claims 1-10 which is a diagnostic composition.

- 67 -

12. The composition of any one of claims 1-10 which is a therapeutic composition.
- 5 13. The composition of any one of claims 1-12 for the manufacture of an agent for detecting and/or verifying, for the treatment, alleviation and/or prevention of metabolic diseases or dysfunctions, including metabolic syndrome, obesity, and/or diabetes, as well as related disorders such as eating disorder, cachexia, hypertension, coronary heart disease, hypercholesterolemia, dyslipidemia, osteoarthritis, or
10 gallstones, in cells, cell masses, organs and/or subjects.
14. Use of a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 nucleic acid molecule, particularly of a nucleic acid molecule according to claim 3 (a), (b) or (c), or a polypeptide
15 encoded thereby or a functional fragment or a variant of said nucleic acid molecule or said polypeptide and/or an effector/modulator of said nucleic or polypeptide for the manufacture of a medicament for the treatment of obesity, diabetes, and/or metabolic syndrome for controlling the function of a gene and/or a gene product which is
20 influenced and/or modified by a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 polypeptide, particularly by a polypeptide according to claim 3.
- 25 15. Use of a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 nucleic acid molecule, particularly of a nucleic acid molecule according to claim 3(a), (b) or (c), or a polypeptide encoded thereby or a functional fragment or a variant of said nucleic acid molecule or said polypeptide or use of an effector/modulator of said nucleic acid molecule or said polypeptide for identifying
30 substances in vitro capable of interacting with a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 polypeptide, particularly with a polypeptide according to claim 3.

- 68 -

16. A non-human transgenic animal exhibiting a modified expression of a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 polypeptide, particularly of a polypeptide according to claim 3.
- 5 17. The animal of claim 16, wherein the expression of the CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 polypeptide, particularly of a polypeptide according to claim 3, is increased and/or reduced.
- 10 18. A recombinant host cell exhibiting a modified expression of a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 polypeptide, particularly of a polypeptide according to claim 3.
19. The cell of claim 18 which is a human cell.
- 15 20. A method of identifying a (poly)peptide involved in the regulation of energy homeostasis and/or metabolism of triglycerides in a mammal comprising the steps of
- 20 (a) contacting a collection of (poly)peptides with a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 polypeptide, particularly of a polypeptide according to claim 3, or a functional fragment thereof under conditions that allow binding of said (poly)peptides;
- (b) removing (poly)peptides which do not bind and
- 25 (c) identifying (poly)peptides that bind to said polypeptide.
21. A method of screening for an agent which modulates/effects the interaction of a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 polypeptide, particularly of a polypeptide according to claim 3, with a binding target, comprising the steps of
- 30 (a) incubating a mixture comprising

- 69 -

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- (aa) a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 polypeptide, particularly of a polypeptide according to claim 3, or a functional fragment thereof;
 - (ab) a binding target/agent of said polypeptide or functional
 - fragment thereof; and
 - (ac) a candidate agent
 - under conditions whereby said polypeptide or functional
 - fragment thereof specifically binds to said binding
 - target/agent at a reference affinity;
 - 10 (b) detecting the binding affinity of said polypeptide or functional
 - fragment thereof to said binding target to determine an
 - affinity for the agent; and
 - (c) determining a difference between affinity for the agent and
 - the reference affinity.

15

22. A method for screening for an agent, which modulates/effects the activity of a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 polypeptide, particularly of a polypeptide according to claim 3, comprising the steps of

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- (a) incubating a mixture comprising
 - (aa) said polypeptide or a functional fragment thereof and
 - (ab) a candidate agent
 - under conditions whereby said polypeptide or functional
 - fragment thereof has a reference activity;
 - 25 (b) detecting the activity of said polypeptide or functional
 - fragment thereof to determine an activity in the presence of
 - the agent; and
 - (c) determining a difference between the activity in the presence
 - of the agent and the reference activity.

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- 70 -

23. A method of producing a composition comprising the (poly)peptide identified by the method of claim 20 or the agent identified by the method of claim 21 or 22 with a pharmaceutically acceptable carrier, diluent and/or additive.
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24. The method of claim 23 wherein said composition is a pharmaceutical composition for preventing, alleviating or treating of metabolic diseases or dysfunctions, including metabolic syndrome, obesity, and/or diabetes, as well as related disorders such as eating disorder, cachexia, hypertension, coronary heart disease, hypercholesterolemia, dyslipidemia, osteoarthritis, or gallstones.
- 10
25. Use of a (poly)peptide as identified by the method of claim 20 or of an agent as identified by the method of claim 21 or 22 for the preparation of a pharmaceutical composition for the treatment, alleviation and/or prevention of metabolic diseases or dysfunctions, including metabolic syndrome, obesity, and/or diabetes, as well as related disorders such as eating disorder, cachexia, hypertension, coronary heart disease, hypercholesterolemia, dyslipidemia, osteoarthritis, or gallstones.
- 15
26. Use of a nucleic acid molecule as defined in any of claims 1-6 or 10 for the preparation of a medicament for the treatment, alleviation and/or prevention of metabolic diseases or dysfunctions, including obesity, diabetes, and/or metabolic syndrome, as well as related disorders such as eating disorder, cachexia, hypertension, coronary heart disease, hypercholesterolemia, dyslipidemia, osteoarthritis, or gallstones.
- 20
27. Use of a polypeptide as defined in any one of claims 1 to 6, 8 or 9 for the preparation of a medicament for the treatment, alleviation and/or prevention of metabolic diseases or dysfunctions, including
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- 30

- 71 -

obesity, diabetes, and/or metabolic syndrome, as well as related disorders such as eating disorder, cachexia, hypertension, coronary heart disease, hypercholesterolemia, dyslipidemia, osteoarthritis, or gallstones.

5

28. Use of a vector as defined in claim 7 or the preparation of a medicament for the treatment, alleviation and/or prevention of metabolic diseases or dysfunctions, including obesity, diabetes, and/or metabolic syndrome, as well as related disorders such as eating disorder, cachexia, hypertension, coronary heart disease, hypercholesterolemia, dyslipidemia, osteoarthritis, or gallstones.

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15

29. Use of a host cell as defined in claim 18 or 19 for the preparation of a medicament for the treatment, alleviation and/or prevention of metabolic diseases or dysfunctions, including obesity, diabetes, and/or metabolic syndrome, as well as related disorders such as eating disorder, cachexia, hypertension, coronary heart disease, hypercholesterolemia, dyslipidemia, osteoarthritis, or gallstones.

20

30. Use of a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 nucleic acid molecule or of a functional fragment thereof for the production of a non-human transgenic animal which over- or under-expresses the CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 gene product.

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30

31. Kit comprising at least one of

- (a) a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 nucleic acid molecule or a functional fragment thereof;
- (b) a CG7956, aralar1, how, CG9373, cpo, Jafrac1, or CG14440 amino acid molecule or a functional fragment thereof;
- (c) a vector comprising the nucleic acid of (a);

- 72 -

- (d) a host cell comprising the nucleic acid of (a) or the vector of (c);
- (e) a polypeptide encoded by the nucleic acid of (a);
- (f) a fusion polypeptide encoded by the nucleic acid of (a);
- 5 (g) an antibody, an aptamer or another effector / modulator against the nucleic acid of (a) or the polypeptide of (b), (e) or (f) and
- (h) an anti-sense oligonucleotide of the nucleic acid of (a).

Figure 1. Triglyceride content of a *Drosophila* CG7956 (GadFly Accession Number) mutant

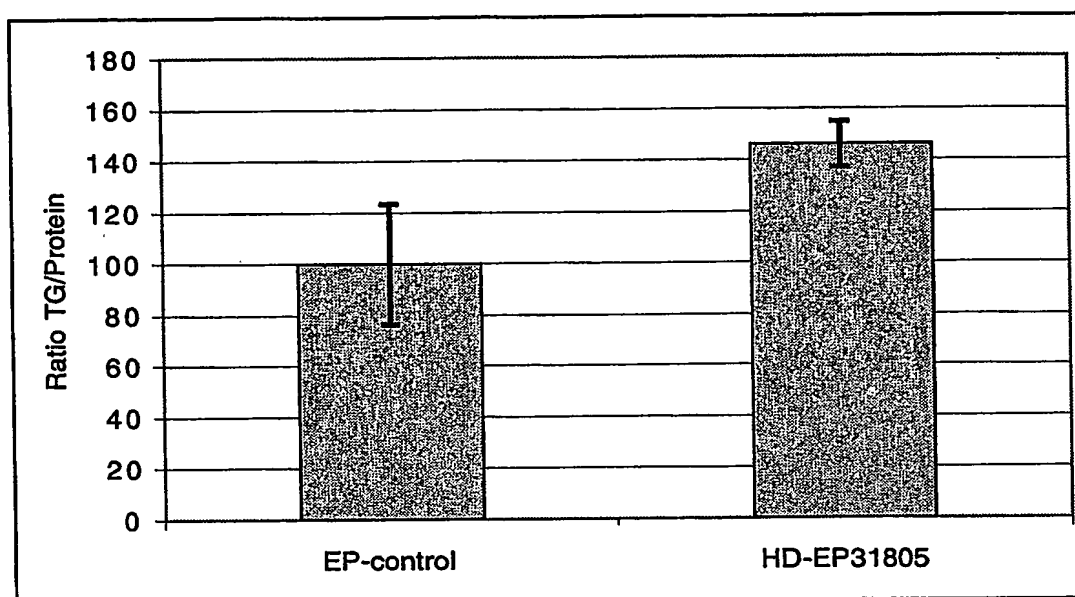


Figure 2. Molecular organization of the CG7956 gene (GadFly Accession Number)

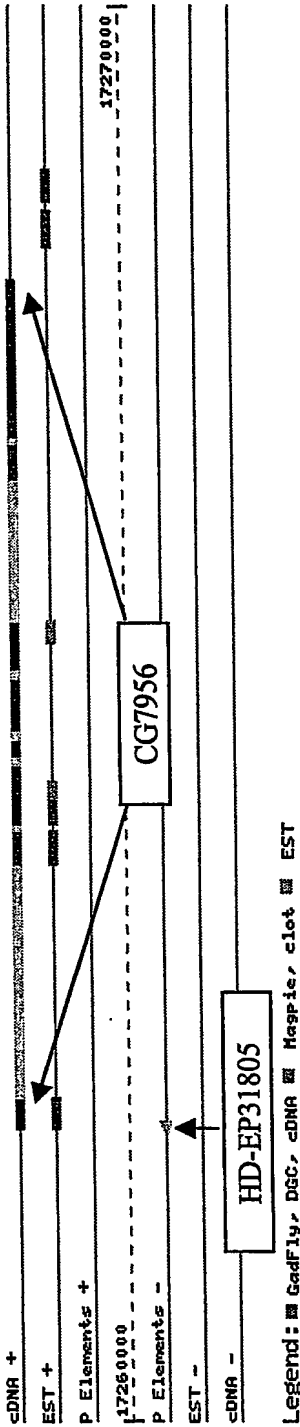


Figure 3. BLASTP results for CG7956 (GadFly Accession Number)**Homology to human protein NP_055752.1 (GenBank Accession Number)**

ref|NP_055752.1| (NM_014937) KIAA0966 protein [Homo sapiens]
Length = 1132

Score = 573 bits (1477), Expect = e-162

Identities = 354/972 (36%), Positives = 514/972 (52%), Gaps = 114/972 (11%)

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Query: 1  MEVFQTDSHYIFVKRDKSLWWHRRRTSEFSIKAGWDLSSVDDIECIGVTHGIVGVISLPNV 60
      ME+FAQ  HYI  + +++LW  RR      ++  DL      +  C+G+  G++G I L  +
Sbjct: 1  MELFQAKDHYILQQGERALWCSRRDGGGLQLRPATDLLLAWNPICLGLVEGVIGIKIQLHSD 60

Query: 61  YEPHLVVVKEASAVGVLYPPHLVYKIKSICILSADD---PDTDLPNCTKHTKSNQSTPTH 117
      L+++++ + VG L   H V K+  I +LS  +      D +L  C KH
Sbjct: 61  LPWWLILIRQKALVGKLPDHEVCKVTKIAVLSLSEMEPQDLELELCCKH----- 110

Query: 118  SVSTSNNNNASVPSSGGGSSKSTKLFEGMNKTWGA VKSAGNT---IKNTTQQAANLATKQ 174
      G+NK      + S  ++      +K  T      +N++
Sbjct: 111  -----HFGINKPEKIIPSPDDSKFLLKTFTHIKSNVSAPN 145

Query: 175  VKSSVGIREPRHIERRITEELHKIFDETDSFYFSFDCDITNNLQRHEAKSEESQ---SQP 231
      K      +E  +ERR+  EEL K+F +++SFY+S  D+TN++QR      +  +  +
Sbjct: 146  KKKVKESKEKEKLERLLEELLKMFMDSESFYYSLT YDLTNSVQRQSTGERDGRPLWQKV 205

Query: 232  DERFFWNKHMIRDLINLNDKT---WILPIIQGFMQVENCVIG----- 270
      D+RFFWNK+MI+DL  +      WI+P+IQGF+Q+E  V+
Sbjct: 206  DDRFFWNKYMIQDLTEIGTPDVDFWIIIPMIQGFVQIEELVVNYTESSDDEKSSPETPPQE 265

Query: 271  NEC-----FTLALVSRRSRHRAGTRYKRRGVDEKGN CAN YVETE QILSFRHHQLSFTQ 323
      + C      F +AL+SRRSRHRAG  RYKRRGVD+  GN  ANYVETE Q++  +H LSF Q
Sbjct: 266  STCVDDIHPRFLVALISR SRHRAGMRYKRRGV DKGNGVANYVETEQLIHVHNHTLSFVQ 325

Query: 324  VRGSVPIYWSQPGYKYRPPPRLD RGV AETQQA FELHFTKELETYGRVCIVNLVEQSGKEK 383
      RGSVP++WSQ  GY+Y P  PRLDR  ET  F  HF  ++L  Y  +  I+NLV+Q+G+EK
Sbjct: 326  TRGSVPVFW SQVGYRYNPRPRLDRSEKETVAYFCAHFEEQLNIYKKQVIINLVDQAGREK 385

Query: 384  TIGDAYADHVIKLNNDRLIYVTFDFHDYCRGMR FENVSALIDAVGPEAGAMGFHWRDQRG 443
      IGDAY  V+  NN  L  YV+FD FH++CRGM+FENV  L  DA+      M  +  W  D+  G
Sbjct: 386  IIGDAYLKQVLLFNNSHLTYVSFDFHEHCRGMKFENVQTLTDAIYDIILDMKWCWVDEAG 445

Query: 444  MICNQKSVFRVNCMDCLDR TNV VQTAIGKAVLESQ LVKLGLSPPYTPIPEQLKSPFMVLW 503
      +IC Q+  +FRVNCMDCLDR TNV VQ  AI  +  V+E  QL  KLG+  PP  P+P  +      +  ++W
Sbjct: 446  VICKQEGIFRVN CMDCLDR TNV VQAAIARV VMEQQLKKLGVMPPPEQPLPVKCNRIYQIMW 505

Query: 504  ANNGDIISRQYAGTNALKGDYTRTGERKISGMMKDG MNSANRYYLARFKDSYRQATIDLM 563
      ANNGD  ISRQYAGT  ALKGD+TRTGERK++G+MKDG+NSANRYYL  RFKD+YRQA  IDLM
Sbjct: 506  ANNGDSISRQYAGTAALKGDFTRTGERKLAGVMKDG VNSANRYYLNRFKDAYRQAVIDLM 565

Query: 564  LGNQVSSESLSALGGQAGPD---ENDGTENAEQAKLLVEDCRLLLGTAQYPVGAWGLID 620
      G  V+  +  S      +  +  +  +  +  E      L++  +LLL  +  G  W  LID
Sbjct: 566  QGIPVTEDLYSIFTKEKEHEALHKENQRSHQELISQLLQSYMKLLLPDDEKFHGGWALID 625

Query: 621  ADPSSGDINETEVD TILLLTDDCYIVA EYDSHLDKIVRFEKVQLTQVRLIELGMHQQT KI 680
      DPS  D      +VD  +LLL++  Y  VA  YD  +DK+  +++++  L  +  IE+G  +  +
Sbjct: 626  CDPSLIDATHRDVDVLLLSNSAYYVAYYDDEV DKNQYQRLSLENLEKIEIG--PEPTL 683

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Query: 681 FQGSAPAHLCRLNYSVDEQEGYFHMFRSANLRFFNNMAYVIKTQEEVAESMTSIVEMFR 740
F P C+RL+Y E GYFH R A + +E+ +++ I EM +
Sbjct: 684 F--GKPKFSCMRLHYRYKEASGYFHTLR-----AVMRNPEEDGKDTLQCIAEMLQ 731

Query: 741 IALDNAGNTEVRYITGGVLQRRKSKLPTLDV-----PRGMPRNLSESQLVQLSSKA 791
I G+ I L+R+ SK P D+ +N S+ L+ K
Sbjct: 732 ITKQAMGSD--LPIIEKKLERKSSK-PHEDIIGIRSQNQGLAQGNFLMSKFSSLNQKV 788

Query: 792 LSNMA----GQFSKLGQTFKKPQAHPSLSAATMNPQVMRQDSEIESGQEA EKAVFTLGR 847
+ G KLG F KP+ + L + + + DS +E+ + V +
Sbjct: 789 KQTKSNVNIGNLRKLG-NFTKPEMKVNFLKPNLKVNLWKS-DSSLETMENT--GVMDKVQ 844

Query: 848 KHRNSNSASSTDTDEHDNSLYEPEVDS DVEIAMDKSNYNE-NAFLPSVGIVMG----NQK 902
+ + +S D+ D L + D D ++A + + LPS GI+ +
Sbjct: 845 AESDGMSSDNDSDYHSDEFLTNSKSDedrQLANSLESVGPIDYVLPSCGIIASAPRLGSR 904

Query: 903 EDSPPSSSDEIRH 914
S SS+D H
Sbjct: 905 SQSLSSTDSSVH 916

Figure 4. Expression of the CG7956 Homologs in Mammalian Tissues
Figure 4A. Real-time PCR analysis of Sac domain-containing inositol phosphatase 2 (SAC2) expression in wild type mouse tissues

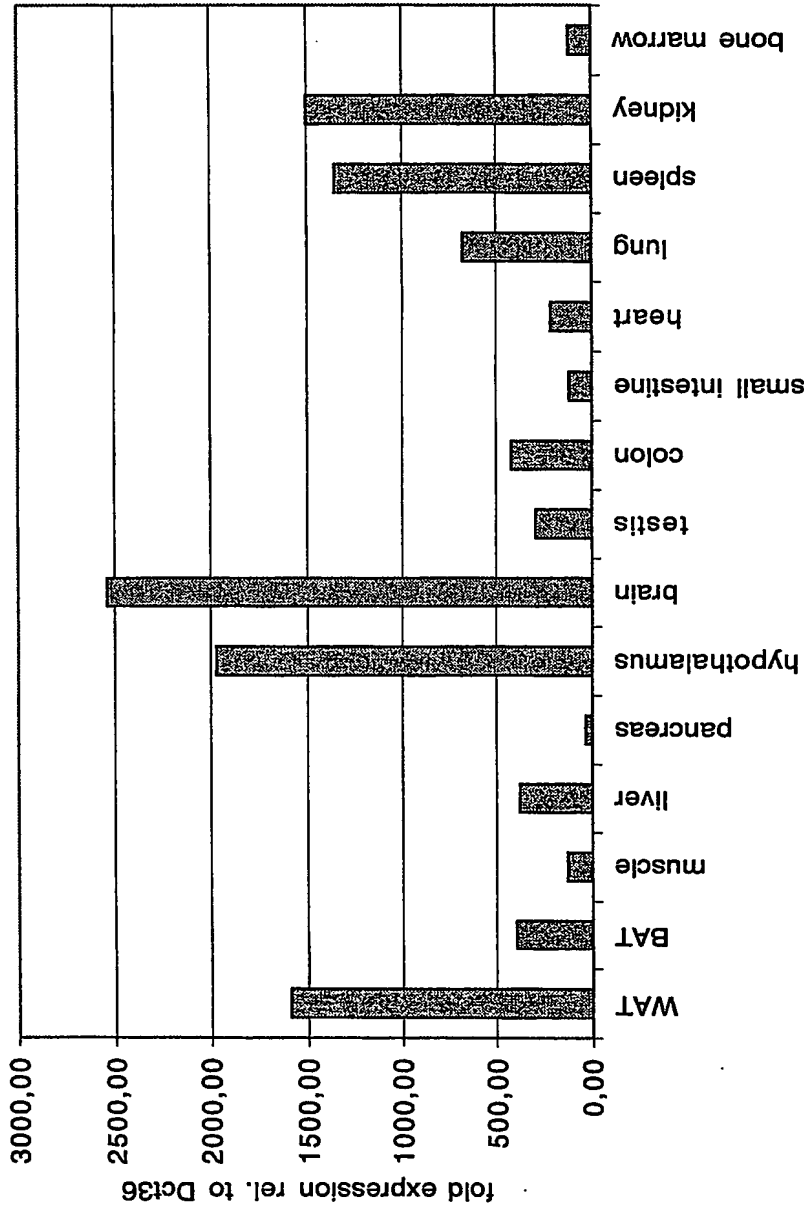


Figure 4B. Real-time PCR analysis of Sac domain-containing inositol phosphatase 2 (SAC2) expression in different mouse models

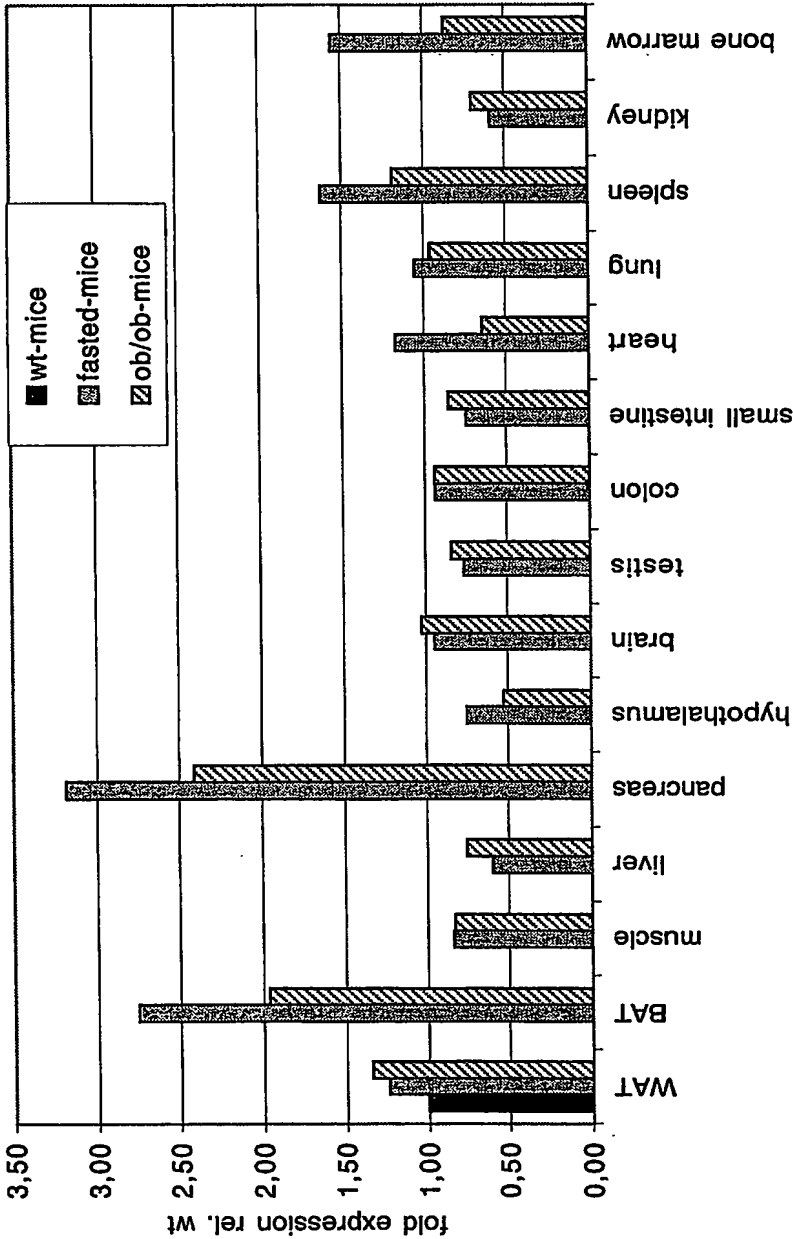


Figure 5. Triglyceride content of a *Drosophila aralar 1* (GadFly Accession Number CG2139) mutant

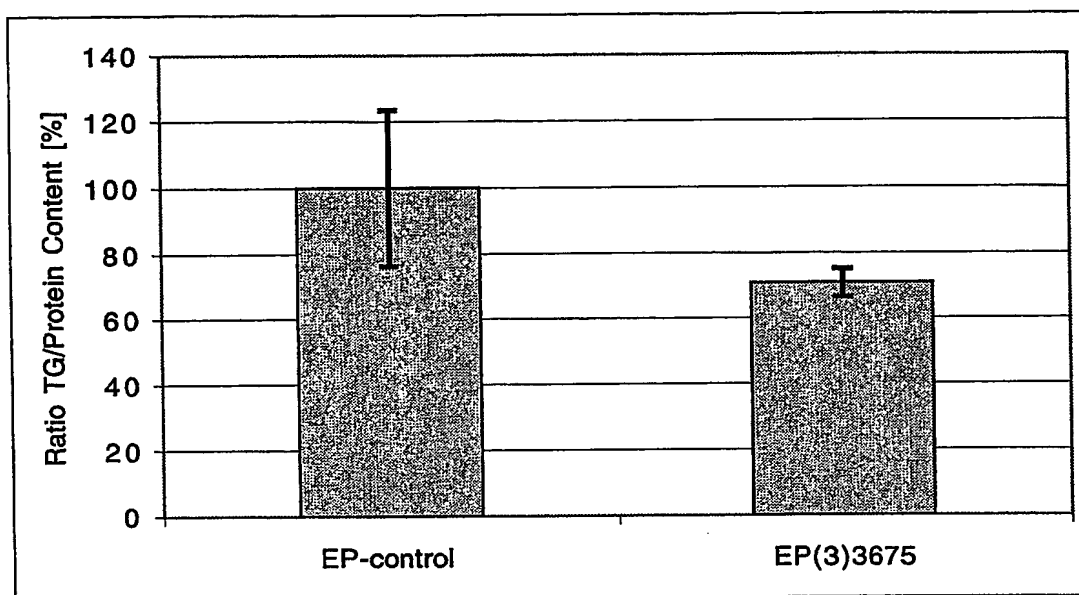


Figure 6. Molecular organisation of the *aralar1* gene (GadFly Accession Number CG2139)

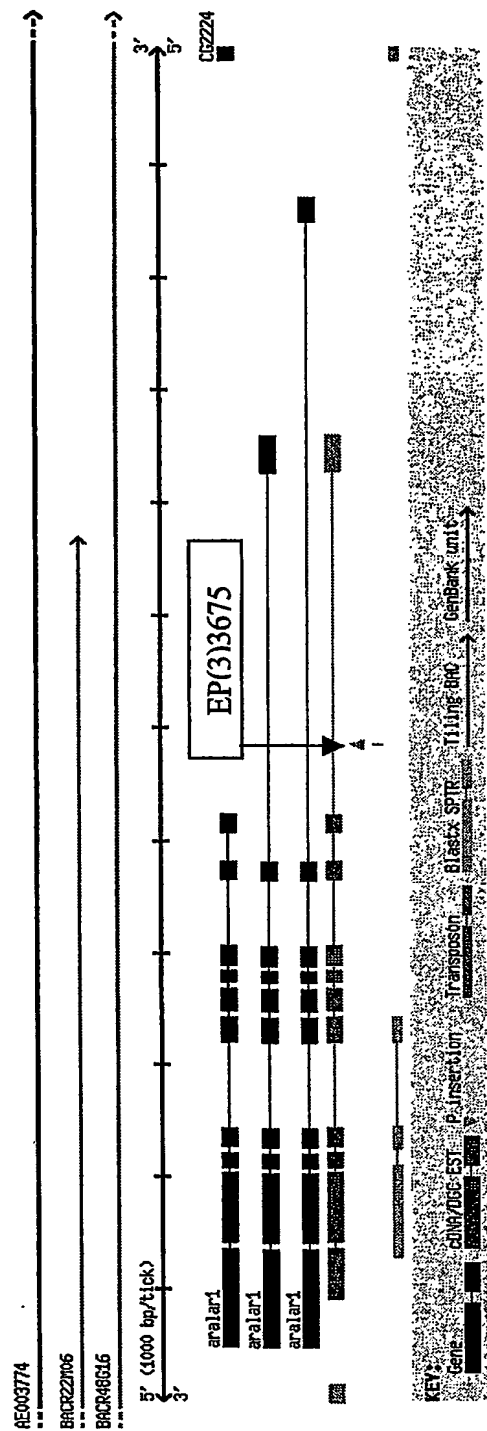


Figure 7. Homology of *Drosophila aralar 1* (GadFly Accession Number CG2139) to human solute carrier family 25, members 12 and 13

Figure 7A. BLASTP results for *alaral 1*

Homology to human protein XP_010876.3 (GenBank Accession Number)

ref|XP_010876.3| (XM_010876) solute carrier family 25 (mitochondrial carrier, Aralar), member 12 [Homo sapiens]
Length = 678

Score = 741 bits (1913), Expect = 0.0

Identities = 382/650 (58%), Positives = 488/650 (74%), Gaps = 14/650 (2%)

```

Query: 1  MTSEDFVRKFLGLFSESASFNDESVRLLANIADTSKDGLISFSEFQAFEGLLCTPDALYRT 60
          MT EDFV+++LGL+++ N + V+LLA +AD +KDGLIS+ EF AFE +LC PD+++
Sbjct: 34  MTPEDFVQRYLGLYNDPNSNPQIVQLLAGVADQTKDGLISYQEFLLAFESVLCAPDSMFIV 93

Query: 61  AFQLFDRKNGTVSYADFADVQKTELHSKIPFSLDGPFIKRYFGDKKQRLINYAEFTQL 120
          AFQLFD+ GNG V++ + ++ +T +H IPF+ D FI+ +FG +++ +NY EFTQ
Sbjct: 94  AFQLFDKSGNGEVTTFENVKEIFGQTTIIHHIPFNWDCEFIRLHFGHNRKKHLNYTEFTQF 153

Query: 121  LHDFHEEHAMEAFRSKDPAGTGFISPLDFQDIIVNVKRHLLTPGVRDNLVSVTEG---HK 177
          L + EHA +AF KD + +G IS LDF DI+V ++ H+LTP V +NLVS G H+
Sbjct: 154  LQELQLEHARQAFALKDKSKSGMISGLDFSDIMVTIRSHMLTPFVEENLVSAAGGSISHQ 213

Query: 178  VSFPFYFIAFTSLNNMELIKQVYLHATEGSRTDM-ITKDQILLAAQTMSQITPLEIDILF 236
          VSF YF AF SLLNNMEL++++Y G+R D+ +TK++ +A Q+TPLEIDIL+
Sbjct: 214  VSFSYFNAFNSLNNMELVRKIY-STLAGTRKDVEVTKEEFAQSAIRYGVQVTPLEIDILY 272

Query: 237  HLAGAVHQAGRIDYSDLSNIAPEHYTKHMTLRLAEIKAVESPA-DRSAFIQVLESSYRFT 295
          LA + +GR+ +D+ IAP + + LAE++ +SP R ++Q+ ES+YRFT
Sbjct: 273  QLADLYNASGRLTLADIERIAPLAEGA-LPYNLAELQRQSPGLGRPIWLQIAESAYRFT 331

Query: 296  LGSFAGAVGATVVPIDLVKTRMQNQ-AGSYIGEYAYRNSWDCFKKVVVRHEGFMGLYRG 354
          LGS AGAVGAT VYPIDLVKTRMQNQ +GS +GE+ Y+NS+DCFKKV+R+EGF GLYRG
Sbjct: 332  LGSVAGAVGATAVYPIDLVKTRMQNQSGSVVGELMYKNSFDCFKKVLRYEGFFGLYRG 391

Query: 355  LLPQLMGVAPEKAIKLTVNDLVKTRDKLTDKKGNIPTWAEVLAGGCAGASQVFTNPLEIVK 414
          L+PQL+GVAPEKAIKLTVND VRDK T + G++P AEVLAGGCAG SQV+FTNPLEIVK
Sbjct: 392  LIPQLIGVAPEKAIKLTVNDFVRDKFTRRDGVSPLPAEVLAGGCAGGSQVIFTNPLEIVK 451

Query: 415  IRLQVAGEIASGSKIRAWSVVRELGLFGLYKGARACLLRDVPFSAIYFPTYAHTKAMMAD 474
          IRLQVAGEI +G ++ A +V+R+LG+FGLYKGA+AC LRD+PFSAIYFP YAH K ++AD
Sbjct: 452  IRLQVAGEITTGPRVSALNVLRDLGIFGLYKGAKACFLRDIPFSAIYFPVYAHCKLLAD 511

Query: 475  KDGYNHPLTLLAAGAIAGVPAASLVTPADVIKTRLQVVARSGQTTYTGVDATKKIMAE 534
          ++G+ L LLAAGA+AGVPAASLVTPADVIKTRLQV AR+GQTTY+GV D +KI+ EE
Sbjct: 512  ENGHVGGLNLLAAGAMAGVPAASLVTPADVIKTRLQVAARAGQTTYSGVIDCFRKILREE 571

Query: 535  GPRAFVKGTAAARVFRSSPQFGVTLVTYELLQRLFYVDFGGTQPKGSEAHKITTPLEQAAA 594
          GP AFWKGTAAARVFRSSPQFGVTLVTYELLQRYFYDFGG +P GSE TP + A
Sbjct: 572  GPSAFVKGTAAARVFRSSPQFGVTLVTYELLQRFYIDFGGLKPAGESE----PTP-KSRIA 626

Query: 595  SVTTENVVDHIGGYRAAVPLLAGVESKFGLYLPFRF-GRGVTAASPSTATGS 643
          + N DHIGGYR A AG+E+KFGLYLP+F V P A +
Sbjct: 627  DLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSVAVVQPKAAVA 676

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Homology to human protein NP_055066.1 (GenBank Accession Number)

ref|NP_055066.1| (NM_014251) solute carrier family 25, member 13 (citrin)
[Homo sapiens]
Length = 675

Score = 728 bits (1878), Expect = 0.0
Identities = 374/643 (58%), Positives = 476/643 (73%), Gaps = 17/643 (2%)

Query: 1 MTSSEDFVRKFLGLFSESAFNDESVRLLANIADTSKDGLISFSEFQAFEGLLCTPDALYRT 60
M+ DFV ++L +F ES N ++V LL+ + D +KDGLISF EF AFE +LC PDAL+
Sbjct: 35 MSPNDFVTRYLNIFGESQPNPKTVELLSGVVDQTKDGLISFQEFVAFESVLCAPDALFMV 94

Query: 61 AFQLFDRKGNGTVSADFAVVQKTELHSKIPFSLDGPFIKRYFGDKKQRLINYAEFTQL 120
AFQLFD+ G G V++ D V +T +H IPF+ D F++ +FG +++R + YAEFTQ
Sbjct: 95 AFQLFDKAGKGEVTFEDVKQVFGQTTIHQHIPFNWDSEFVQLHFGKERKRHLTYAEFTQF 154

Query: 121 LHDFHEEHAMEAFRSKDPAGTGFIPLDFQDIIVNVKRHLLTPGVRDNLVSVTEG---HK 177
L + EHA +AF +D A TG ++ +DF+DI+V ++ H+LTP V + LV+ G H+
Sbjct: 155 LLEIQLEHAKQAFVQORDNARTGRVTAIDFRDIMVTIRPHVLTFFVEECLVAAAGGTTSHQ 214

Query: 178 VSFPYFIAFTSLLNNMELIKQVYLHATEGSRTDM-ITKDQILLAAQMSQITPLEIDILF 236
VSF YF F SLLNNMELI+++Y G+R D+ +TK++ +LAAQ Q+TP+E+DILF
Sbjct: 215 VSFSYFNGFNSSLNNMELIRKIY-STLAGTRKDVEVTKEEFVLAAQKFGQVTPMEVDILF 273

Query: 237 HLAGAVHQAGRIDYSDLSNIAP-EHYTKHMTHLAEIKAVESPAD--RSAFIQVLESSYR 293
LA GR+ +D+ IAP E T + LAE + ++ D R +QV ES+YR
Sbjct: 274 QLADLYEPRGRMTLADIERIAPLEBGT--LPFNLAEAQRQKASGDSARPVLLQVAESAYR 331

Query: 294 FTLGSFAGAVGATVVYPIDLVKTRMQNQRA-GSYIGEVAIRNSWDCFKKVVREHGFMGly 352
F LGS AGAVGAT VYPIDLVKTRMQNQRA+ GS++GE+ Y+NS+DCFKKV+R+EGF GLY
Sbjct: 332 FGLGSVAGAVGATAVYPIDLVKTRMQNQRTSGSFVGLMYKNSFDCFKKVLRYEGFFGLY 391

Query: 353 RGLLPQLMGVAPEKAIKLTVNDLVRDKLTDKKGNIPTWAEVLAGGCAGASQVFTNPLEI 412
RGLLPQL+GVAPEKAIKLTVND VRDK K G++P AE+LAGGCAG SQV+FTNPLEI
Sbjct: 392 RGLLPQLLGVAPKAIAIKLTVNDFVRDKFMHKDGSVPLAAEILAGGCAGGSQVIFTNPLEI 451

Query: 413 VKIRLQVAGEIASGSKIRAWSVVRELGLFGLYKGARACLLRDVPFSAIYFPTYAHTKAMM 472
VKIRLQVAGEI +G ++ A SVVR+LG FG+YKGA+AC LRD+PFSAIYFP YAH KA
Sbjct: 452 VKIRLQVAGEITTGPRVSALSVVRDLGFFGIYKGAKACFLRDIPFSAIYFPCYAHVKASF 511

Query: 473 ADKDGYNHPLTLAAGAIAGVPAASLVTPADVIKTRLQVVARSGQTTYTGVDATKKIMA 532
A++DG P +LL AGAIAG+PAASLVTPADVIKTRLQV AR+GQTTY+GV D +KI+
Sbjct: 512 ANEDGQVSPGSLLLAGAIAGMPAASLVTPADVIKTRLQVAARAGQTTYSGVIDCFRKILR 571

Query: 533 EEGPRAFWKGTAAARVFRSSPQFGVTLVITYELLQRLFYVDFGGTQPKGSEAHKITTPLEQA 592
EEGP+A WKG ARVFRSSPQFGVTL+TYELLQR FY+DFGG +P GSE P+ ++
Sbjct: 572 EEGPKALWKAGARVFRSSPQFGVTLITYELLQRWFYIDFGGVKPMGSE-----PVPKS 625

Query: 593 AASVTTENVDHIGGYRAAVPLLAGVESKFGLYLPRFGRGVTA 635
++ N DH+GGY+ AV AG+E+KFGLYLP F V+ +
Sbjct: 626 RINLPAPNPDHVGKYKLAVATFAGIENKFGLYLPLFKPSVSTS 668

Figure 7B. Multiple Sequence Alignment (ClustalW 1.83)

```

aralar1 Dm  MPLTKSLPNSPSLKLAGTEKLRVFLKYASIQKNGEHYMTSEDFVRKFLGLFSESANFND
SLC25A12 Hs  -----MAVKVQTTKRQDPHELNRNIFLQYASTEVDGERYMTPEDFVQRYLGLYNDPNSNP
SLC25A13 Hs  -----MAAAKVALTKRADPAELRTIFLKYASIEKNGEFFMSPNDFVTRYLNIFGESQPNP

aralar1 Dm  ESVRLLANIADTSKDGLISFSEFQAFEGLLCTPDALYRTAFQLFDRKGNGTVSYADFADV
SLC25A12 Hs  KIVQLLAGVADQTKDGLISYQEFLLAFESVLCAPDSMFIVAFQLFDKSGNGEVTTFENVKEI
SLC25A13 Hs  KTVELLSGVVDQTKDGLISFQEFVAFESVLCAPDALFMVAFQLFDKAGKGEVTFEDVKQV

aralar1 Dm  VQKTELHSKIPFSLDGPFIKRYFGDKKQRLINYAEFTQLLHDFHEEHAMEAFRSKDPAGT
SLC25A12 Hs  FGQTIHHHIPFNWDCEFIHLHFGHNRRKHLNYTEFTQFLQELQLEHARQAFALKDKSKS
SLC25A13 Hs  FGQTTIHQHIFPNWDSEFVQLHFGKERKRHLTYAEFTQFLLEIQLEHAKQAFVQRDNART

aralar1 Dm  GFISPLDFQDIIVNVKRHLLTPGVRDNLVSVTEG---HKVSFPYFIAFTSLLNNMELIKQ
SLC25A12 Hs  GMISGLDFSDIMVTIRSHMLTPFVEENLVSAAAGGSIHQVSFSYFNAFNSLLNNMELVRK
SLC25A13 Hs  GRVTAIDFRDIMVTIRPHVLTTPFVEECLVAAAGGTTSHQVSFSYFNGFNSLLNNMELIRK

aralar1 Dm  VYLHATEGSRTDMITKDQILLAAQTMSQITPLEIDILFHLGAVHQAGRIDYSDLNIAPI
SLC25A12 Hs  IYSTLAGTRKDVEVTKEEFAQSAIRYGQVTPLEIDILYQLADLYNASGRLTLADIERIAPI
SLC25A13 Hs  IYSTLAGTRKDVEVTKEEFVLAQAQFGQVTPMEVDILFQLADLYEPRGRMTLADIERIAPI

aralar1 Dm  EHYTKHMTTHRLAEIKAVESPA--DRSAFIQVLESSYRFTLGSFAGAVGATVVYPIDLVKT
SLC25A12 Hs  LAEG-ALPYNLAELQRQQSPG-LGRPIWLQIAESAYRFTLGSVAGAVGATAVYPIDLVKT
SLC25A13 Hs  LEEG-TLPFNLAEAQRQKASGDSARPVLLQVAESAYRFTLGSVAGAVGATAVYPIDLVKT

aralar1 Dm  RMQNQR-AGSYIGEVAIRNSWDCFKKVVRHEGFMGLYRGLLPQLMGVAPEKAIKLTVNDF
SLC25A12 Hs  RMQNQRGSGSVVGELMYKNSFDCFKKVLRYEGFFGLYRGLIPQLIGVAPEKAIKLTVNDF
SLC25A13 Hs  RMQNQRSTGSFVGELMYKNSFDCFKKVLRYEGFFGLYRGLLPQLLGVAPKAIKLTVNDF

aralar1 Dm  VRDKLTDKKGNIPTWAEVLAGGCAGASQVFTNPLEIVKIRLQVAGEIASGSKIRAWSVV
SLC25A12 Hs  VRDKFTRRDGSVPLPAEVLAGGCAGGSQVIFTNPLEIVKIRLQVAGEITTGPRVSALNVL
SLC25A13 Hs  VRDKFMHKDGSVPLAAEILAGGCAGGSQVIFTNPLEIVKIRLQVAGEITTGPRVSALSIV

aralar1 Dm  RELGLFGLYKGARACLLRDVPFSAIYFPTYAHTKAMMADKDGYNHPLTLAAGAIAGVPA
SLC25A12 Hs  RDLGIFGLYKGAKACFLRDIPFSAIYFPVYAHCKLLADENGHVGGNLNLLAAGAMAGVPA
SLC25A13 Hs  RDLGFFGIYKGAKACFLRDIPFSAIYFPCYAHVKASFANEDGQVSPGSLLLAGAIAGMPA

aralar1 Dm  ASLVTPADVVIKTRLQVVARSGQTTYTGVDATKKIMAEEGPRAFWKGTAARVFRSSPQFG
SLC25A12 Hs  ASLVTPADVVIKTRLQVAARAGQTTYSGVIDCFRKILREEGPSAFWKGTAAARVFRSSPQFG
SLC25A13 Hs  ASLVTPADVVIKTRLQVAARAGQTTYSGVIDCFRKILREEGPKALWKAGARVFRSSPQFG

aralar1 Dm  VTLVITYELLQRLFYVDFGGTQPKGSEAHKITTPLEQAAAASVTTENVDHIGGYRAAVPLLA
SLC25A12 Hs  VTLVITYELLQRWFYIDFGGLKPAGSEP----TPKSRIAD-LPPANPDHIGGYRLATATFA
SLC25A13 Hs  VTLITYELLQRWFYIDFGGVKPMGSEP----VPKSRIIN--LPAPNPDHVGGYKLAVATFA

aralar1 Dm  GVESKFGLYLPRFGRGVTAASPSTATGS---
SLC25A12 Hs  GIENKFGLYLPKFKSPSVAVVQPKAAVAATQ
SLC25A13 Hs  GIENKFGLYLPLFK-PSVSTSKAIGGGP---
```

Figure 8. Expression of *aralar 1* Homologs in Mammalian Tissues

Figure 8A. Real-time PCR analysis of Slc25a12 expression in wild type mouse tissues (DCt Pancreas = 18,94)

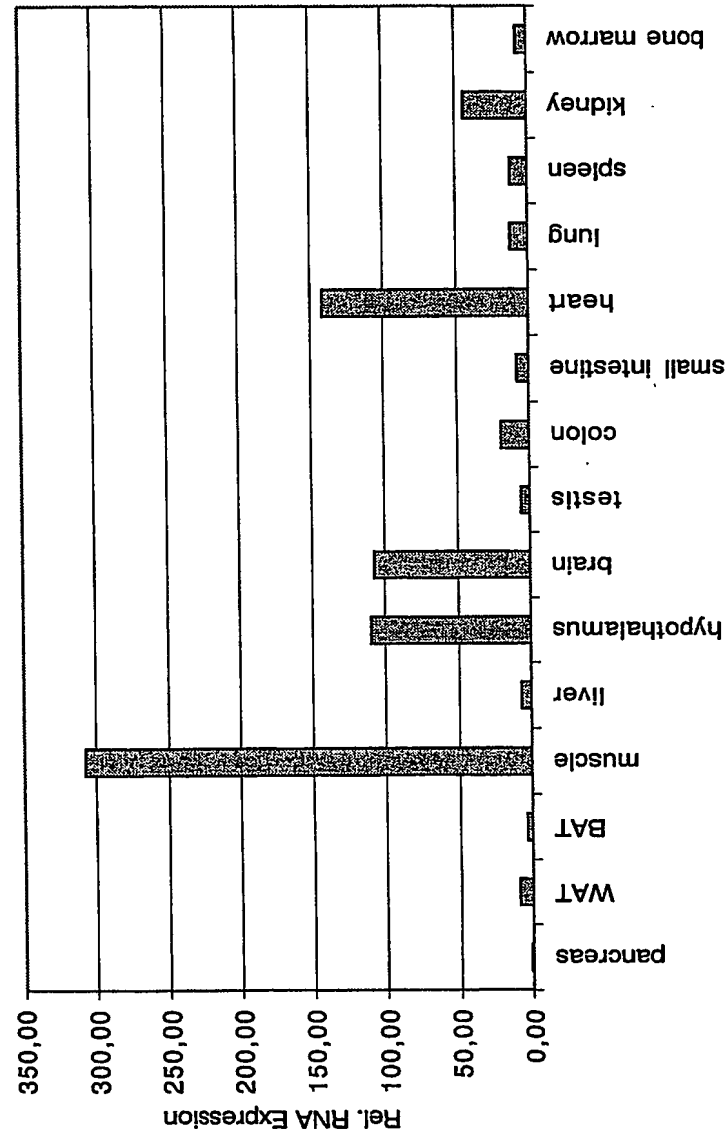


Figure 8B. Real-time PCR analysis of Slc25a12 expression in different mouse models

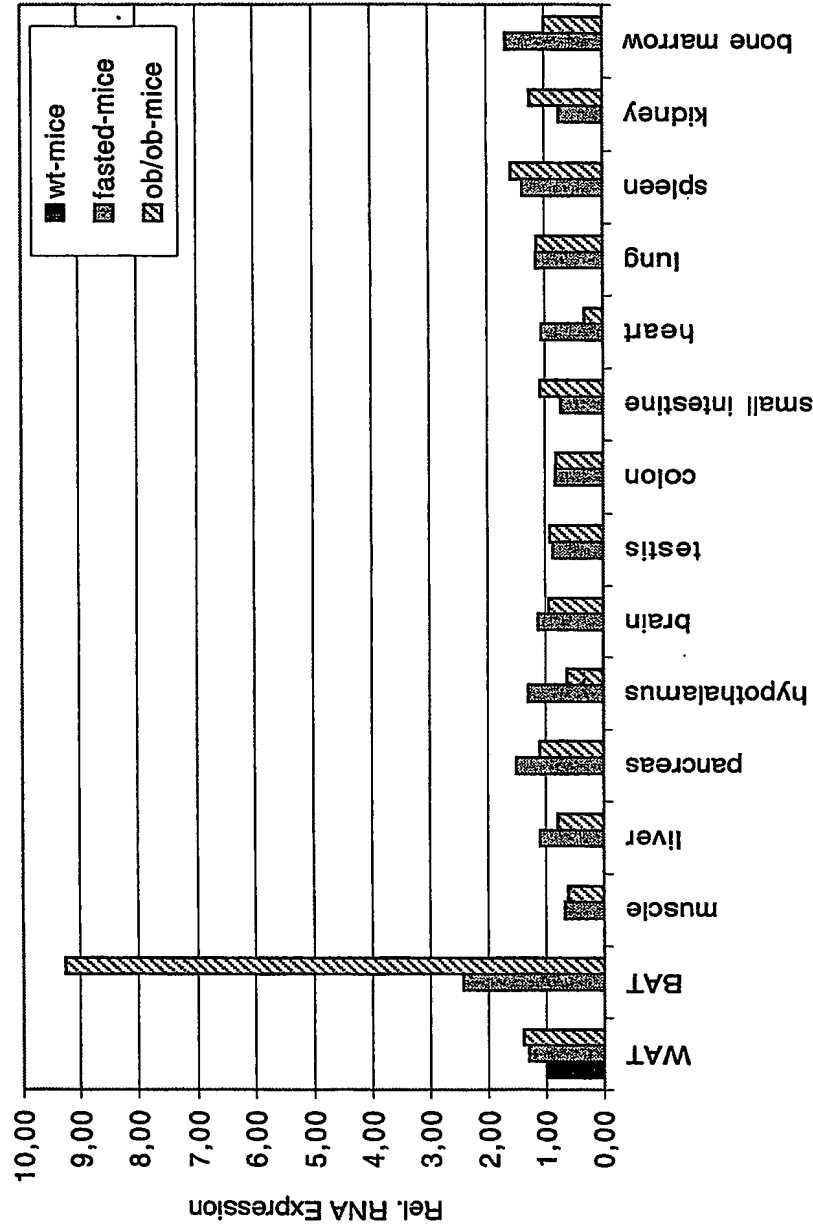


Figure 8C. Real-time PCR analysis of Slc25a13 expression in wild type mouse tissues (DCt Pancreas = 20,41)

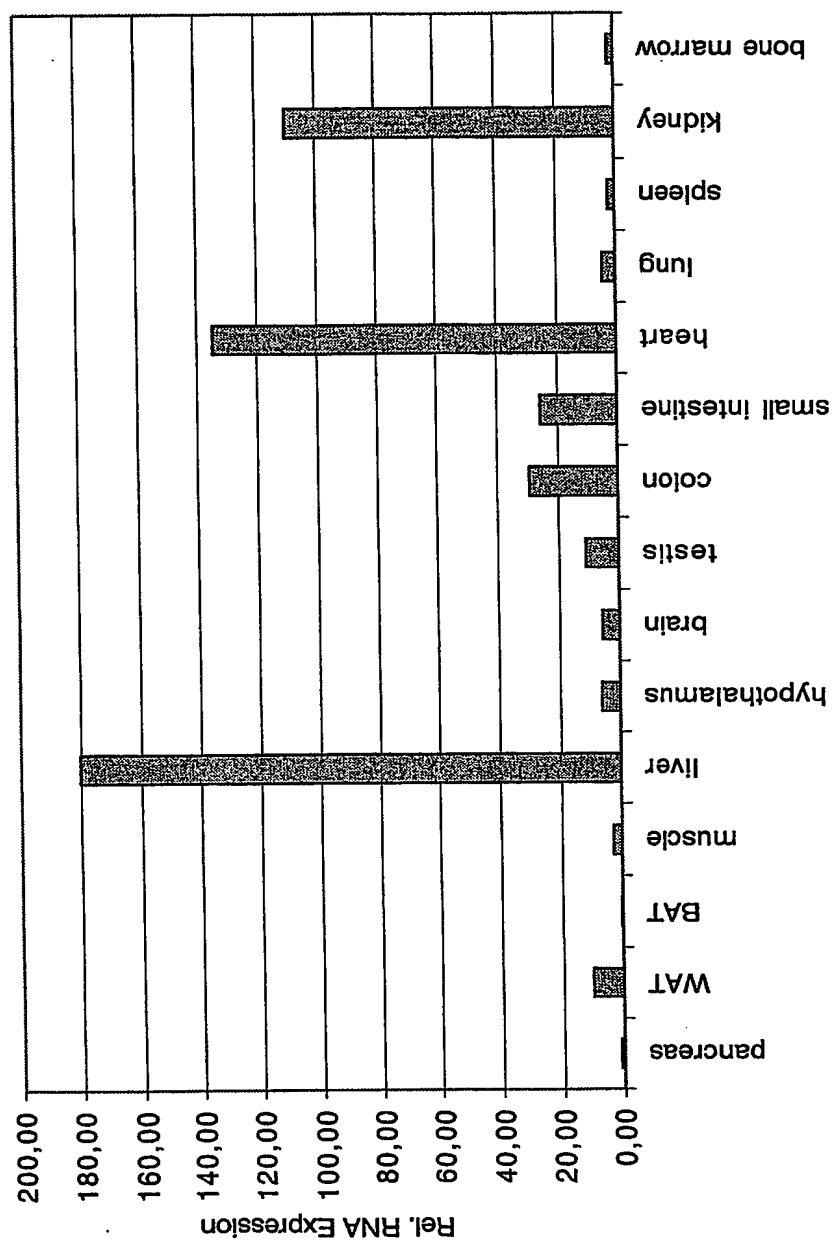


Figure 8D. Real-time PCR analysis of Slc25a13 expression in in different mouse models

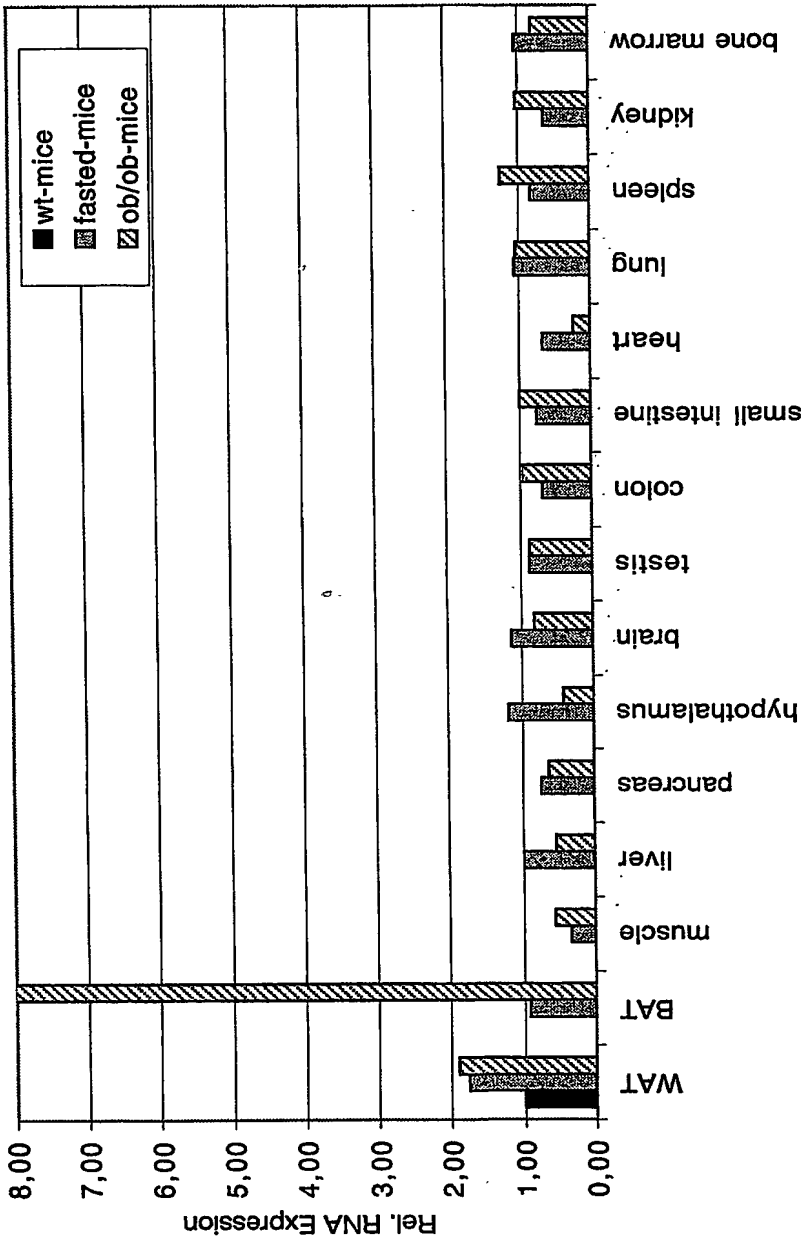


Figure 9. Triglyceride content of a *Drosophila how* (GadFly Accession Number CG10293) mutant

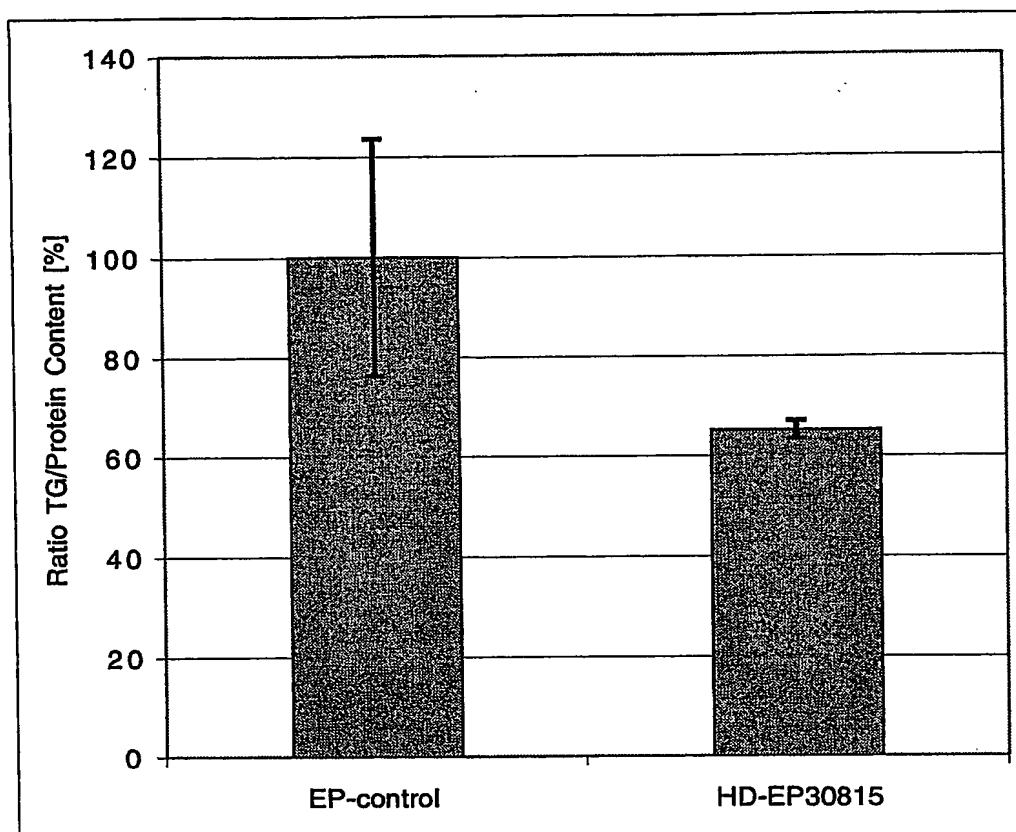


Figure 10. Molecular organisation of the *how* gene (GadFly Accession Number CG10293)

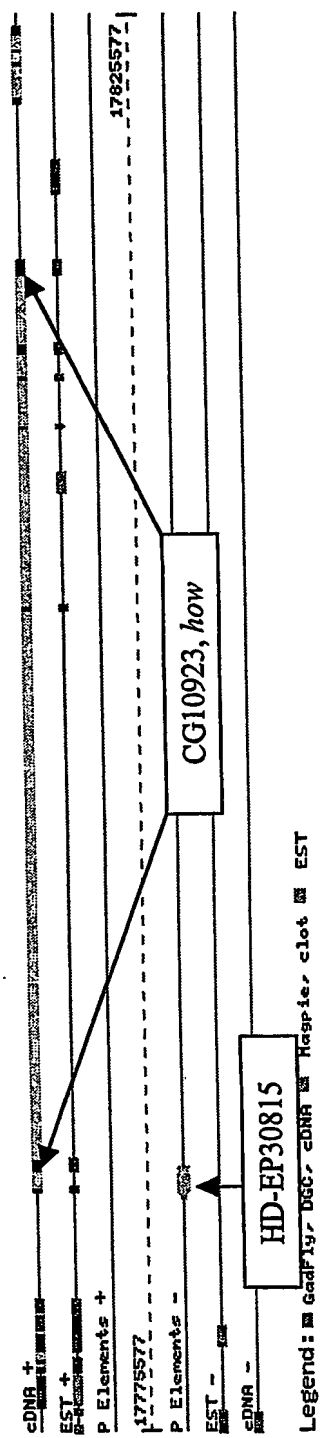


Figure 11. Homology of *Drosophila how* (GadFly Accession Number CG10293) to human Quaking isoforms

Figure 11A. BLASTP results for CG10293 (GadFly Accession Number)

gb|AAF63416.1|AF142421_1 (AF142421) QUAKING isoform 5 [Homo sapiens]
Length = 337

Score = 289 bits (739), Expect = 5e-77
Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 2 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 62 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHLVITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHLVITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 122 KGSMRDKKKEQNRGKPNWEHLNEDLHLVITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 182 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 239

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357
P A P PLI + V + + PTAA G G+I+ PY+Y Y
Sbjct: 240 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 292

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389
+L + S +GA+ + R R HPYQR
Sbjct: 293 ATSILEYPIEPSGVLGAVATKVRHRDMRVHPYQR 326

ref|XP_037438.2| (XM_037438) similar to KH domain RNA binding protein QKI-5A [Homo sapiens], Length = 341

Score = 289 bits (739), Expect = 5e-77
Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHLVITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHLVITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 126 KGSMRDKKKEQNRGKPNWEHLNEDLHLVITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 243

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357
 P A P PLI + V + + PTAA G G+I+ PY+Y Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 296

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389
 +L + S +GA+ + R R HPYQR
 Sbjct: 297 ATSILEYPIEPSGVLGAVATKVRHRDMRVHPYQR 330

gb|AAF63414.1|AF142419_1 (AF142419) QUAKING isoform 6 [Homo sapiens]
 Length = 363

Score = 289 bits (739), Expect = 5e-77
 Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 28 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 88 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQEVQKLLVPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 148 KGSMRDKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRABEIKLKRAVEEVKLLVPAAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAPALRT 265

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357
 P A P PLI + V + + PTAA G G+I+ PY+Y Y
 Sbjct: 266 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 318

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389
 +L + S +GA+ + R R HPYQR
 Sbjct: 319 ATSILEYPIEPSGVLGAVATKVRHRDMRVHPYQR 352

dbj|BAB55032.1| (AK027309) unnamed protein product [Homo sapiens]
 Length = 323

Score = 282 bits (722), Expect = 5e-75
 Identities = 165/320 (51%), Positives = 208/320 (64%), Gaps = 20/320 (6%)

Query: 81 QLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-VKKEPLTLPEPEGSV 134
 QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG +K LP+ G +
 Sbjct: 2 QLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGSTEKRSAELPDAVGPI 61

Query: 135 VTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRGKGSMRDKKKEDANR 194
 V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRGKGSMRDKKKE+ NR
 Sbjct: 62 VQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRGKGSMRDKKKEQNR 121

Query: 195 GKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQEVQKLLVPQAEGEDELKKRQLMELAI 254
 GKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEGED LKK QLMELAI
 Sbjct: 122 GKPNWEHLNEDLHVLITVEDAQNRABEIKLKRAVEEVKLLVPAAEGEDSLKKMQLMELAI 181

Query: 255 INGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRAPA-AAPLGAPLILN 313
 +NGTYRD KS A+ A + R++T A +R P A P PLI
 Sbjct: 182 LNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRTPTPAGPTIMPLIRQ 239

Query: 314 PRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALAGNPLLTEYADHS-- 369
 + V + + PTAA G G+I+ PY+Y Y +L + S
 Sbjct: 240 IQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY-PYTLAPATSILEYPIEPSGV 292

Query: 370 VGAIKQQRRLATNREHPYQR 389
 +GA+ + R R HPYQR
 Sbjct: 293 LGAVATKVRHRDMRVHPYQR 312

gb|AAF63413.1|AF142418_1 (AF142418) QUAKING isoform 2 [Homo sapiens]
 Length = 347

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 28 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 88 EKRSaelPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEOVKLLVPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 148 KGSMRDKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 208 EDslkKQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 265

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 266 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 312

gb|AAF63417.1|AF142422_1 (AF142422) QUAKING isoform 3 [Homo sapiens]
 Length = 341

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 28 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 88 EKRSaelPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEOVKLLVPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 148 KGSMRDKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 265

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 266 PTFAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYFY 312

gb|AAF63415.1|AF142420_1 (AF142420) QUAKING isoform 4 [Homo sapiens]
 Length = 315

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 2 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 62 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQKLLVPAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 122 KGSMRDKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 182 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 239

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 240 PTFAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYFY 286

dbj|BAB69497.1| (AB067799) RNA binding protein HQK-6 [Homo sapiens]
 Length = 319

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQKLLVPAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 126 KGSMRDKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 243

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
P A P PLI + V + + PTAA G G+I+ PY+Y
Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

dbj|BAB69499.1| (AB067801) RNA binding protein HQK-7B [Homo sapiens]
Length = 319

Score = 280 bits (716), Expect = 2e-74
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 66 EKRSaelPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 126 KGSMRDKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 243

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
P A P PLI + V + + PTAA G G+I+ PY+Y
Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

dbj|BAB69498.1| (AB067800) RNA binding protein HQK-7 [Homo sapiens]
Length = 325

Score = 280 bits (716), Expect = 2e-74
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 66 EKRSaelPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 126 KGSMRDKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 243

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
P A P PLI + V + + PTAA G G+I+ PY+Y
Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

gb|AAF63412.1|AF142417_1 (AF142417) QUAKING isoform 1 [Homo sapiens]
Length = 321

Score = 280 bits (716), Expect = 2e-74
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 2 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 62 EKRSaelPDavgPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQKLLVPPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 122 KGSMRDKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 182 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 239

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
P A P PLI + V + + PTAA G G+I+ PY+Y
Sbjct: 240 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 286

dbj|BD004960.1| Genes related to stomach cancer, Length = 1993

Score = 288 bits (738), Expect = 1e-77
Identities = 168/324 (51%), Positives = 211/324 (64%), Gaps = 11/324 (3%)
Frame = +1

Query: 77 DYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-VKKEPLTLPEP 130
DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG +K LP+
Sbjct: 4 DYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGSTEKRSaelPDA 183

Query: 131 EGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRGKGSMRDKKKE 190
G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRGKGSMRDKKKE
Sbjct: 184 VGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRGKGSMRDKKKE 363

Query: 191 DANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQKLLVPPQAEGEDELKKRQLM 250
+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEGED LKK QLM
Sbjct: 364 EQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAGEDSLKKMQLM 543

Query: 251 ELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRAPA-AAPLGAP 309
ELAI+NGTYRD KS A+ A + R++T A +R P A P P
Sbjct: 544 ELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRTPTPAGPTIMP 717

Query: 310 LILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALAGNPLLTEYAD 367
LI + V + + PTAA G G+I+ PY+Y Y +L +
Sbjct: 718 LIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAPATSILEYPIE 876

Query: 368 HS--VGAIKQRRRLATNREHPYQR 389
S +GA+ + R R HPYQR
Sbjct: 877 PSGVLGAVATKVRHDMRVHPYQR

CG10293 Dm MSVCEKAVVQQQLQQHLQQQAAAAVVAAQQQQAQAQAQAQQQQQAPQVVVPMPTP
QKI-6 Hs -----MLSLSSLRNRNSGRNSGSCGAWN-----
QKI-2 Hs -----MLSLSSLRNRNSGRNSGSCGAWN-----
QKI-3 Hs -----MLSLSSLRNRNSGRNSGSCGAWN-----
HOK-7B Hs -----

CG10293 Dm QHLTPQQQQQSTQSIADYLAQLLKDRKQLAAFPV---VFTHVERLLDEEIIARVRASLF--
QKI-6 Hs -MVGEMETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDDEEISRVRKDMYND
QKI-2 Hs -MVGEMETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDDEEISRVRKDMYND
QKI-3 Hs -MVGEMETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDDEEISRVRKDMYND
HOK-7B Hs -MVGEMETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDDEEISRVRKDMYND

CG10293 Dm QING-VKKEPLTLPEPEGSVVTMNEKVYPVPREHPDFNFVGRILGPRGMTAKQLEQETGC
QKI-6 Hs TLNGSTEKRSAPLDAVGPVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGC
QKI-2 Hs TLNGSTEKRSAPLDAVGPVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGC
QKI-3 Hs TLNGSTEKRSAPLDAVGPVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGC
HOK-7B Hs TLNGSTEKRSAPLDAVGPVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGC

CG10293 Dm KIMVRGKGSMDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLL
QKI-6 Hs KIMVRGKGSMDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLL
QKI-2 Hs KIMVRGKGSMDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLL
QKI-3 Hs KIMVRGKGSMDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLL
HOK-7B Hs KIMVRGKGSMDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLL

CG10293 Dm VPQAEGEDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGL
QKI-6 Hs VPAAEGEDSLKKMQLMELAILNGTYRDANIKSPALAFSLAATAQAAP--RIITGPAPVLP
QKI-2 Hs VPAAEGEDSLKKMQLMELAILNGTYRDANIKSPALAFSLAATAQAAP--RIITGPAPVLP
QKI-3 Hs VPAAEGEDSLKKMQLMELAILNGTYRDANIKSPALAFSLAATAQAAP--RIITGPAPVLP
HOK-7B Hs VPAAEGEDSLKKMQLMELAILNGTYRDANIKSPALAFSLAATAQAAP--RIITGPAPVLP

CG10293 Dm AAQIRAP-AAAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYA
QKI-6 Hs PAALRTPTPAGPTIMPLIR-----QIQTAVMPNGTTPHTAAIVPPGPEAGLIYTPYEYP
QKI-2 Hs PAALRTPTPAGPTIMPLIR-----QIQTAVMPNGTTPHTAAIVPPGPEAGLIYTPYEYP
QKI-3 Hs PAALRTPTPAGPTIMPLIR-----QIQTAVMPNGTTPHTAAIVPPGPEAGLIYTPYEYP
HOK-7B Hs PAALRTPTPAGPTIMPLIR-----QIQTAVMPNGTTPHTAAIVPPGPEAGLIYTPYEYP

CG10293 Dm NYAALAGNPLLTEYADHSVGAIKQORRLATNREHPYQRATVGVPAKPAGFIEIQ
QKI-6 Hs --YTLAPATSILEYPIEPSGVLGAVATKVRHRDMRVHPYQRIVTADRAATGN--
QKI-2 Hs --YTLAPATSILEYPIEPSGVLWEIEMFVMP-DISAH-----
QKI-3 Hs --YTLAPATSILEYPIEPSGVLGMAFPK-----
HOK-7B Hs --YTLAPATSILEYPIEPSGVLGKFFSPWG-----

Figure 12. Expression of human *hox* homologs in mammalian (human) tissue

Figure 12A. Quantitative analysis of Quaking 6 (QKI-6) expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

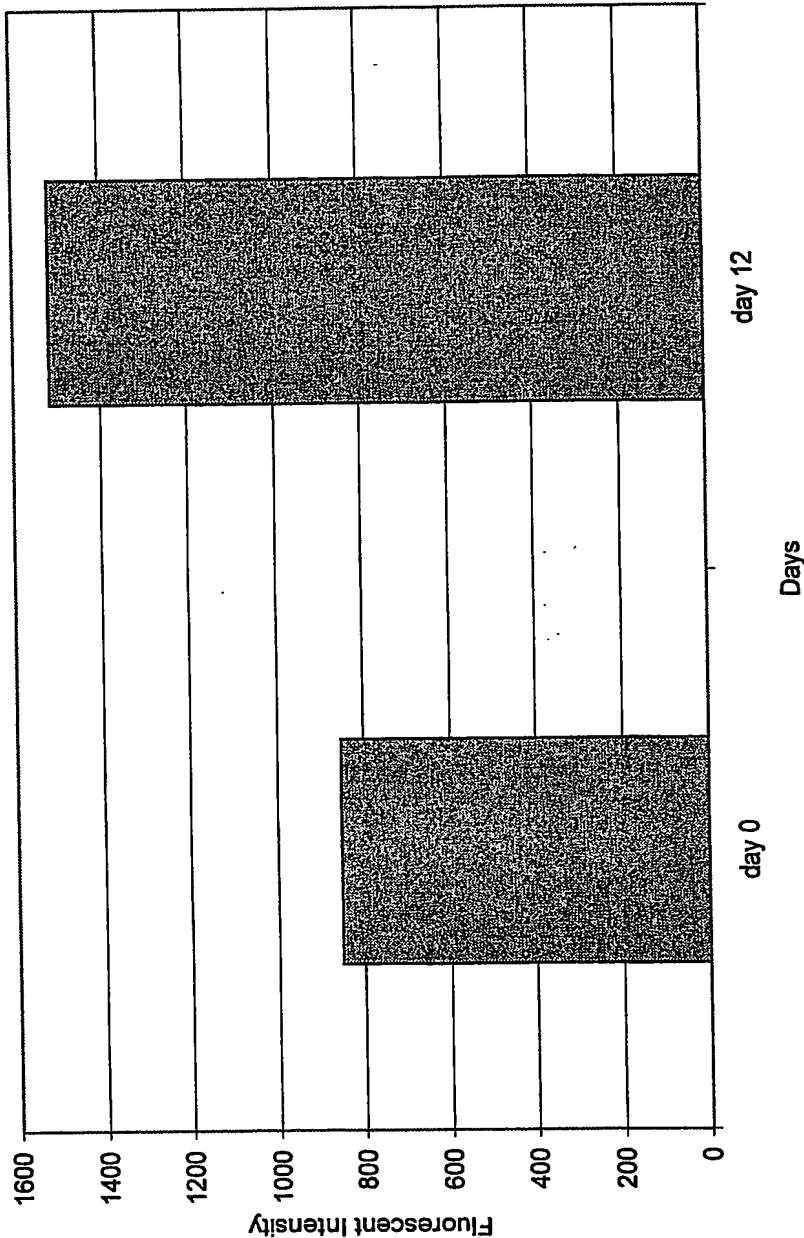


Figure 12B. Quantitative analysis of human RNA binding protein HQK-7B expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

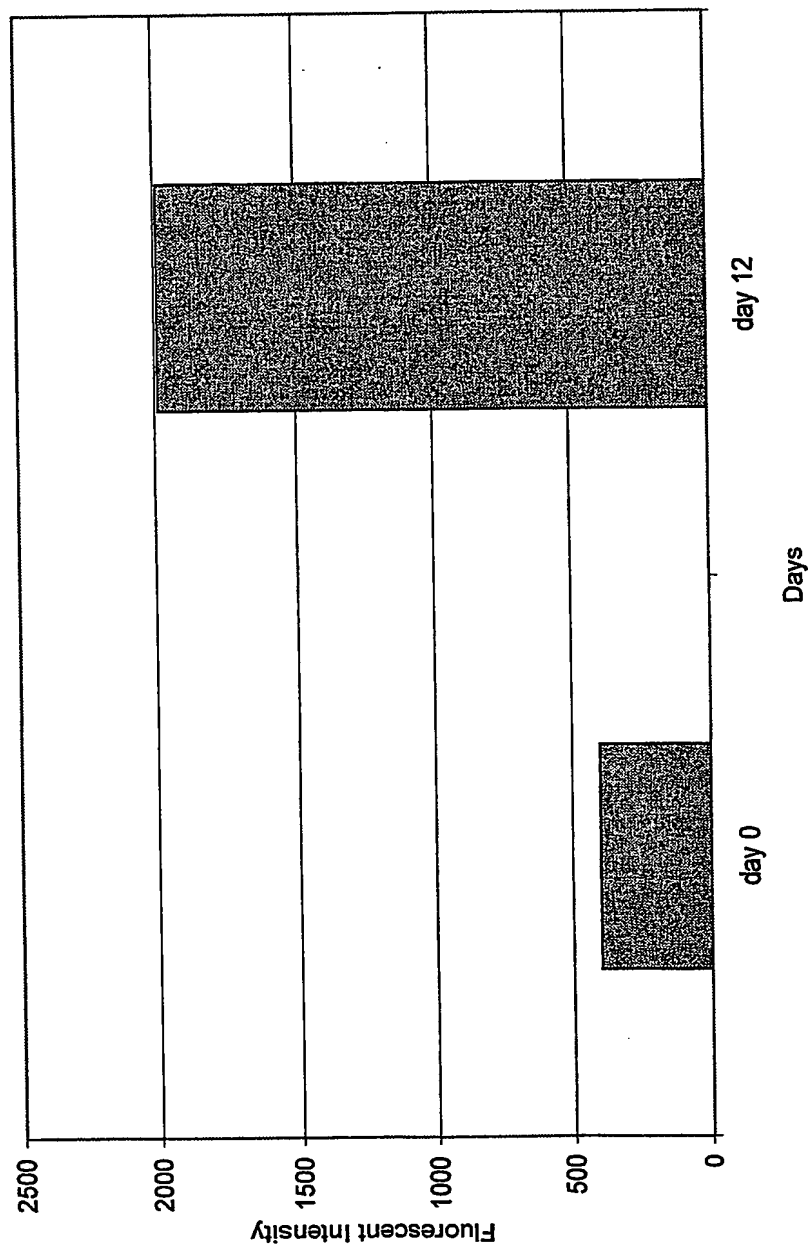


Figure 13. Triglyceride content of a *Drosophila* CG9373 (GadFly Accession Number) mutant

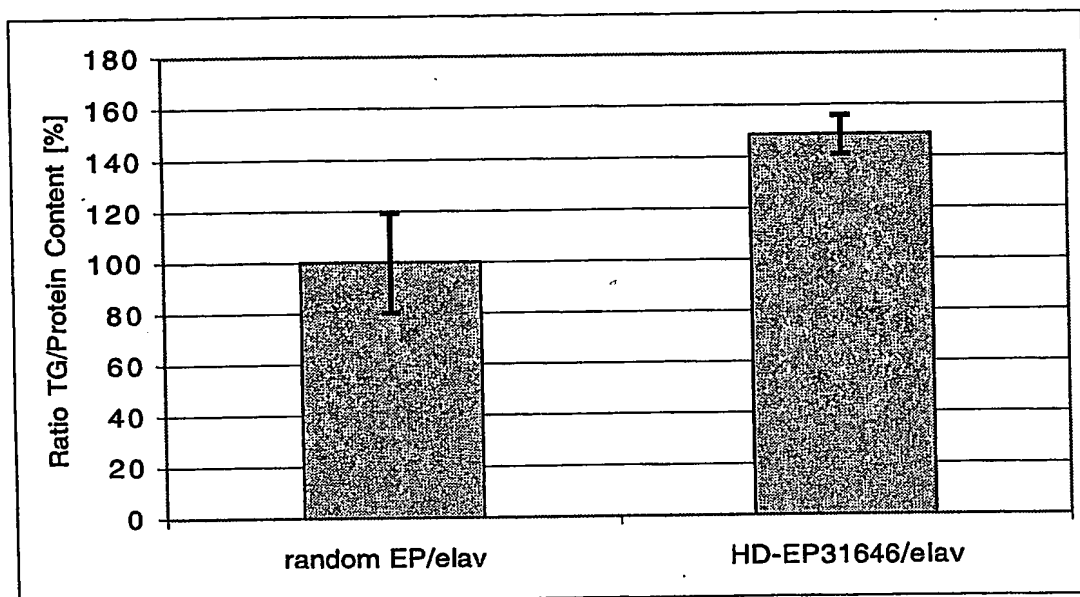


Figure 14. Molecular organisation of the CG9373 gene (GadFly Accession Number)

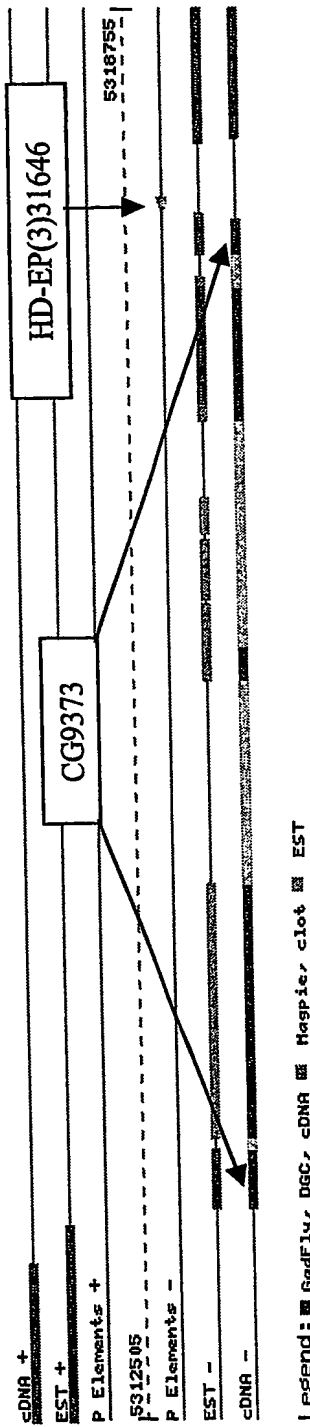


Figure 15. Homology of Drosophila GadFly Accession Number CG9373 to human KIAA1443 protein, human unnamed protein product, and human myelin gene expression factor 2

**Figure 15A. BLASTP results for GadFly Accession Number CG9373
Homology to human protein BAA92579.1 (GenBank Accession Number)**

dbj|BAA92579.1| (AB037762) KIAA1341 protein [Homo sapiens], Length = 620

Score = 249 bits (635), Expect = 1e-64

Identities = 207/660 (31%), Positives = 295/660 (44%), Gaps = 148/660 (22%)

```

Query: 1  MSMDASNSVESREKERDRRGRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCR 58
      + M+  S + + + + G++ +RF + N G G + G RN R
Sbjct: 72  VKMENDESAAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-R 121

Query: 59  VYISNIPYDYRWQDLKDLFRRIVGSIIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKM 118
      V+ISNIPYD +WQ +KDL R VG + YV+LF D GK+RGCG+VEFKD E V+KALE M
Sbjct: 122 VFISNIPYDMKWQAIKDLMREKVGEVTVYVELFKDAEGKSRGCGVVEFKDEEFVKKALETM 181

Query: 119  NRYEVNGRELNVKEDHGEQRDQYGRIVRDGGGGGGGGGGVQGGNGGNNGGGGGGGRDHMD 178
      N+Y+++GR L +KED + + + R GG GG H+
Sbjct: 182 NKYDLSGRPLNIKEDPDGENARRA-LQRTGGSFPGG-----HVP 219

Query: 179  DRDRGFSRRDDRLSGRNNFNMMSSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFVAN 238
      D G L NN N+ +N +G L + +FVAN
Sbjct: 220 DMGSGLMNLPPSIL---NNPNIPPEVISNLQ-----AGRLGSTIFVAN 259

Query: 239  LDYKVDNKKLKQVFKLAGKVQSVDLSDKEGNSRGFAVIEYDHPVEAVQAISMLDRQMLF 298
      LD+KV KKLK+VF +AG V+ D+ DK+G SRG + ++ +EAVQAISM + Q LF
Sbjct: 260 LDFKVGWKKLKEVFSTAGTVKRADIKEDKDGRSGMGTVTTFEQAIEAVQAISMFNGQFLF 319

Query: 299  DRRMTVRLD--RIPDK-----NEGIKLPEGLGGVGIGLGPNGEPLRDVAHNLNPGGQSQ 350
      DR M V++D +P + + +LP GLGG+G+GLGP G+P+ N+
Sbjct: 320 DRPMHVKMDDKSVPHIEYRSHDGKTPQLPRGLGGIGMGLPGGQPISASQLNI----- 372

Query: 351  GQLLGNAQQGSQQLGSVGSQPNSSAVSNATTNLLNNLTGVMFGNHAAPVQSPVAPVQKPSL 410
      G ++GN G + G FG +
Sbjct: 373 GGVMGNLGPGGM-----GMDGPGFGG-----MNRI 397

Query: 411  GNNTGSGGLNLLNLPNPSILAAVVGNLGNQG--GNLSNPLLSSSL-----SNLGLNLGNS 462
      G G GGL N +G G G G L ++SS+ ++G+N G
Sbjct: 398 GGGIGFGGLEAMN-----SMGGFGGVGRMGELYRGAMTSSMERDFGRGDIGINRGFG 449

Query: 463  GNDDNLPPSNVGLSNNYSSGGTGGGNSYSSGNNYSGGGGSSN-----LGYNAYSSS-G 514
      + L + +G +G G N G+ SGG GS N +G + SSS
Sbjct: 450 DSFGRLGSAMIG----GFAGRIGSSNMGPVGSGISGGMGSMNSVTGGMGMLDRMSSSFD 505

Query: 515  GMGGGNGGVVDGNDYNTGNPLDVYGGGNSVGNNSVGSANAVGASRKSDTIKKNVPITC 574
      MG G G + D + G G G +GS K + I ++N+P
Sbjct: 506 RMGPGIGAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLPPFDL 554

Query: 575  TWQTLRDKFREIGDVKFAEI-----RGNDVGVRFFKERDAELALALMDGSRLDGRNIKV 629
      TWQ L++KF + G V FAEI + G VRF AE A +M+G ++ GR I V
Sbjct: 555 TWQKLKEKFSQCGHVMFAEIKMENGKSKGCGTVRFDSPEAEKACRIMNGIKISGREIDV 614

```

Score = 68.6 bits (166), Expect = 2e-10
Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: 20 GRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNCRVYISNIPYDVRWQDLKDLFRR 79
G GA R D D G +G G G+ R+R + N +++ N+P+D WQ LK+ F +
Sbjct: 510 GIGAILERSIDMD-RGFLSGPMGSGM--RERIGSKGN-QIFVRNLPFDLTWQKLKEKFSQ 565

Query: 80 IVGSIEYVQLFFDESCKARGCGIVEFKDPENVQKALEKMNRYEVNGRELNVKED 133
G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D
Sbjct: 566 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPESAEEKACRIMNGIKISGREIDVRLD 617

Score = 56.2 bits (134), Expect = 1e-06
Identities = 46/180 (25%), Positives = 76/180 (41%), Gaps = 21/180 (11%)

Query: 139 DQYGRIVRDGGGGGGG-----GGGVQGGNGGNGGGGGGGGRDHMDRDRGFSRRD 188
D +GR+ GG G G G+ GG G N GG G +D F R
Sbjct: 450 DSFGRLGSAMIGGFAGRIGSSNMGPVSGISGGMGSMNSVTGGMGMG-LDRMSSSFDRM- 507

Query: 189 DDRLSGRNNFNMMSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFFVANLDYKVDNKKL 248
G ++ + + + + E +G G N++FV NL + + +KL
Sbjct: 508 -----GPGIGAILERSIDMDRGFLSGPMGSGMRERIGSKG--NQIFVRNLPFDLTWQKL 559

Query: 249 KQVFKLAGKVQSVDSLSDKEGNSRGFAVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308
K+ F G V ++ ++ G S+G + +D P A +A +++ + R + VRLDR
Sbjct: 560 KEKFSQCGHVMFAEIKMEN-GKSKGCGTVRFDSPESAEEKACRIMNGIKISGREIDVRLDR 618

Homology to human protein BAB14421.1 (GenBank Accession Number)

>dbj|BAB14421.1| (AK023133) unnamed protein product [Homo sapiens],
Length = 576

Score = 242 bits (618), Expect = 1e-62
Identities = 206/654 (31%), Positives = 289/654 (43%), Gaps = 160/654 (24%)

Query: 1 MSMDASNSVESREKERDRRGRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCR 58
+ M+ S + + + + G++ +RF + N G G + G RN R
Sbjct: 52 VKMENDESAAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-R 101

Query: 59 VYISNIPYDVRWQDLKDLFRRIVGSIEYVQLFFDESCKARGCGIVEFKDPENVQKALEKM 118
V+ISNIPYD +WQ +KDL R VG + YV+LF D GK+RGCG+VEFKD E V+KALE M
Sbjct: 102 VFISNIPYDMKWQAIKDLMEKVGVEVTVYELFKDAEGKSRGCGVVEFKDEEFVKKALETM 161

Query: 119 NRYEVNGRELNVKED-HGEQRDQYGRIVRDGGGGGGGGGGGVQGGNGGNGGGGGGGGRDHM 177
N+Y+++GR L +KED GE + + R GG GG H+
Sbjct: 162 NKYDLSGRPLNIKEDPDGENARRASQ--RTGGSFPGG-----HV 198

Query: 178 DDDRGFSRRDDRLSGRNNFNMMSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFFVA 237
D G L NN N+ +N +G L + +FVA
Sbjct: 199 PDMGSGLMNLPPSIL---NNPNIPPEVISNLQ-----AGRLGSTIFVA 238

Query: 238 NLDYKVDNKKLKQVFKLAGKVQSVDSLSDKEGNSRGFAVIEYDHPVEAVQAISMLDRQML 297
NLD+KV KKLK+VF +AG V+ D+ DK+G SRG + ++ +EAVQAISM + Q L
Sbjct: 239 NLDKFKVGWKKLKEVFSIAGTVKRAKEDKDGKSRGMGTVTTFEQAIEAVQAISMFGQFL 298

Query: 298 FDRRMTVRLD--RIPDK-----NEGIKLPEGLGGVGIGLGPNGEPLRDVAHNLPNGGQS 349

FDR M V++D +P + + +LP GLGG+G+GLGP G+P+ N+
 Sbjct: 299 FDRPMHVKMDDKSVPH E EYRSHD G K T P Q L P R G L G G I G M G L G P G G Q P I S A S Q L N I----- 352
 Query: 350 QGQLLGNAQQGSQ L G S V G S Q P N S S A V S N A T T N L L N N L T G V M F G N H A A V Q P S P V A P V Q K P S 409
 G ++GN G + G FG
 Sbjct: 353 -GGVMGNLGP GGM-----GMDGP GFGG-----MNR 376
 Query: 410 LGNNTGSGGLN L N N L N P S I L A A V V G N L G N Q G--GNLSNPLLS S S L-----SNLGLNLGN 461
 +G G GGL N +G G G G L ++SS+ ++G+N G
 Sbjct: 377 IGGGIGFGGLEAMN-----SMGGFGGVGRMGEL YRGAMTSSMERDFGRGDIGINRG- 427
 Query: 462 SGND D N L P P S N V G L S N N Y S S G G T G G G S N Y S S G N N Y S G G G G S S N L G Y N A Y S S S -G M G G G N 520
 G S G G G G N S + G +G + S S S M G G
 Sbjct: 428 -----F G D S F G R L G G G M G M N S V T-----G M G M G L D R M S S S F D R M G P G I 467
 Query: 521 G G V G V D G N D Y T G N P L D V Y G G G S N V G S N V G S A N A V G A S R K S D T I I I K N V P I T C T W Q T L R 580
 G + D + G G G +G S K + I ++N+P T W Q L +
 Sbjct: 468 G A I L E R S I D M D R G F L S G P M G S G M---R E R I G S-----K G N Q I F V R N L P F D L T W Q K L K 516
 Query: 581 D K F R E I G D V K F A E I-----R G N D V G V V R F F K E R D A E L A I A L M D G S R L D G R N I K V 629
 +K F + G V F A E I + G V R F A E A +M+G ++ G R I V
 Sbjct: 517 E K F S Q C G H V M F A E I K M E N G K S K G C G T V R F D S P E S A E K A C R I M N G I K I S G R E I D V 570

Score = 72.8 bits (177), Expect = 1e-11

Identities = 82/348 (23%), Positives = 133/348 (37%), Gaps = 96/348 (27%)

Query: 54 R R N C R V Y I S N I P Y D Y R W Q D L K D L F R R I V G S I E Y V Q L F F D E S G K A R G C G I V E F K D P E N V Q K 113
 R ++++N+ + W+ LK++F I G+++ + D+ GK+RG G V F+ +
 Sbjct: 230 R L G S T I F V A N L D F K V G W K K L K E V F S -I A G T V K R A D I K E D K D G K S R G M G T V T F E Q A I E A V Q 288
 Query: 114 A L E K M N R Y E V N G R E L V V K E D-----H G E Q R D Q Y G R I V R D G G G G G G G----- 155
 A+ N + R + V K D H E R G+ + G G G G
 Sbjct: 289 A I S M F N G Q F L F D R P M H V K M D D K S V P H E E Y R S H D G K T P Q L P R G L G G I G M G L G P G G Q P I S A S 348
 Query: 156 -----G G V Q G-----G N G G N N G G G G-----G G R D H M D D R D R G F 184
 G G V G G G G G N G G G G G M + R G
 Sbjct: 349 Q L N I G G V M G N L G P G G M G M D G P G F G G M N R I G G G I G F G G L E A M N S M G G F G G V G R M G E L Y R G A 408
 Query: 185 S R R D D D R L S G R N N F N M M S-----N D Y N S S N Y N L Y G L S A S F L E S L G--- 225
 +R G R + + N L +S+SF + +G
 Sbjct: 409 M T S S M E R D F G R G D I G I N R G F G D S F G R L G G G M G M N S V T G G M G M G L D R M S S S F -D R M G P G I 467
 Query: 226 -----I S G P L H-----N K V F V A N L D Y K V D N K K L K Q V F K L A G K V Q S 260
 +S G P+ N++FV NL + + +K L K+ F G V
 Sbjct: 468 G A I L E R S I D M D R G F L S G P M G S G M R E R I G S K G N Q I F V R N L P F D L T W Q K L K E K F S Q C G H V M F 527
 Query: 261 V D L S L D K E G N S R G F A V I E Y D H P V E A V Q A I S M L D R Q M L F D R R M T V R L D R 308
 ++ ++ G S+G + +D P A +A +++ + R + V R L D R
 Sbjct: 528 A E I K M E N -G K S K G C G T V R F D S P E S A E K A C R I M N G I K I S G R E I D V R L D R 574

Score = 68.6 bits (166), Expect = 2e-10

Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: 20 G R G A R G S R F T D A D G N G N G A G S Q G G G V A A R D R S R E R R N C R V Y I S N I P Y D Y R W Q D L K D L F R R 79
 G G A R D D G +G G G+ R+R + N ++++ N+P+D W Q L K+ F +
 Sbjct: 466 G I G A I L E R S I D M D -R G F L S G P M G S G M---R E R I G S K G N -Q I F V R N L P F D L T W Q K L K E K F S Q 521
 Query: 80 I V G S I E Y V Q L F F D E S G K A R G C G I V E F K D P E N V Q K A L E K M N R Y E V N G R E L V V K E D 133

G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D
 Sbjct: 522 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPESAEEKACRIMNGIKISGREIDVRLD 573

Homology to human protein NP057216.1 (GenBank Accession Number)

ref|NP_057216.1| (NM_016132) myelin gene expression factor 2 [Homo sapiens]
 gb|AAD43038.1| (AF106685) myelin gene expression factor 2 [Homo sapiens]
 Length = 547

Score = 238 bits (607), Expect = 2e-61

Identities = 204/659 (30%), Positives = 295/659 (43%), Gaps = 150/659 (22%)

Query: 3 MDASNSVESREKERDRRGGRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCRVY 60
 M+ S + + + + G++ +RF + N G G + G RN RV+
 Sbjct: 1 MENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-RVF 50

Query: 61 ISNIPYDYRWQDLKDLFRRIVGSI EYVQLFFDES GKARGCGIVEFKDPENVQKALEKMNR 120
 ISNIPYD +WQ +KDL R VG + YV+LF D GK+RGCG+VEFKD E V+KALE MN+
 Sbjct: 51 ISNIPYDMKWQA IKDL MREKVGEV TYVELFKDAEGKSRGCGVVEFKDEEFVKKALETMNK 110

Query: 121 YEVNGREL VVKEDHGEQRDQYGRIVRDGGGGGGGGGGVQGGNGGNNGGGGGGGRDHMDDR 180
 Y+++GR + +KED + + + R G QG + + G G
 Sbjct: 111 YDLSGRRVNIKEDPDGENARRA-LQRTGTS-----FQGS HASDVGSG----- 151

Query: 181 DRGFSRRDDRLSGRNNFNMMSSNDYNNSSNYNLYGLSASFLES LGISGPLHNKVFVANLD 240
 N+ + NN + + + +L +G L + +FVANLD
 Sbjct: 152 -----LVNLPSSILNNPN-----IPPEVISNLQ-AGRLGSTIFVANLD 188

Query: 241 YKVDNKKLKQVFKLAGKVQSVDSL DKEGNSRGFAVIEYDHPVEAVQAISM LDRQMLFDR 300
 +KV KKLK+VF +AG V++ DK+G SRG + ++ +EAVQAISM + Q LFDR
 Sbjct: 189 FKVGWKKLKEVF SIAGTVKAGSYKEDKDGKSRGMGTVTTFEQAI EAVQAISM FNGQFLFDR 248

Query: 301 RMTVRLD-----RIPDKNEG IKLPEGLGGVGIGLGPNGEPLRDVAHNLPNGGQSQG 351
 M V++D R PD + +LP GLGG+G+GLGP G+P+ N+ G
 Sbjct: 249 PMHVKMDDKSV PHEEYRSPD-GKTPQLPRGLGGIGMGLGPGGQPISASQLNI-----G 300

Query: 352 QLLGNAQQGSQLGSGVSGQPNS SAVSNATTNLLNLTGV MFGNHA AVQSPVAPVQKPSLG 411
 ++GN G + G FG +G
 Sbjct: 301 GVMGNLGP GGM-----GMDGPGFGG-----MNRIG 325

Query: 412 NNTGSGGLNLLNLP SILAAVGNLGNQG--GNLSNPLLSSSL S-----NLGLNLGN SG 463
 G GGL N +G G G G L ++SS+ ++GL+ G
 Sbjct: 326 GGIGFGGLEAMN-----SMGGFGGVGRMGEL YRGAMTSSMERDFGHRDIGLSRGFGD 377

Query: 464 NDDNLPPSNVGLSN NYSSGGTGGGNSYSSGN NYSGGGGSSN-----LGYNAYSSS-GG 515
 + L + +G +G G N G+ SGG GS N +G + SSS
 Sbjct: 378 SFGR LGSAMIG----GITGRIGSSNMGPV GSGISGGMGSMNSVTGGMGMLDRMSSSFDR 433

Query: 516 MGGGNGGVGVGDNDYNTGNPLDVYGGGSGNVGNSNVGSANAVGASRKSDTII IKNPITCT 575
 MG G G + D + G G G +GS K + I ++N+P T
 Sbjct: 434 MGP GIGAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLPFDLT 482

Query: 576 WQTLRDKFREIGDV KFAEI-----RGNDVG VVRFFKERDAELAIALMDGSR LDGRNIKV 629
 WQ L++KF + G V FAEI + G VRF AE A +M+G ++ GR I V
 Sbjct: 483 WQKLKEKFSQCGHVMFAEIKMENGKSKGCGTVRF DSPESAEEKACRIMNGIKISGREIDV 541

Score = 68.6 bits (166), Expect = 2e-10
Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: 20 GRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNCRVYISNIPYDYRWQDLKDLFRR 79
G GA R D D G +G G G+ R+R + N +++ N+P+D WQ LK+ F +
Sbjct: 437 GIGAILERSIDMD-RGFLSGPMGSGM--RERIGSKGN-QIFVRNLPFDLTWQKLKEKFSQ 492

Query: 80 IVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNRVEVNGRELVVKED 133
G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D
Sbjct: 493 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPEAEKACRIMNGIKISGREIDVRLD 544

Score = 55.5 bits (132), Expect = 2e-06
Identities = 41/157 (26%), Positives = 69/157 (43%), Gaps = 11/157 (7%)

Query: 152 GGGGGGVQGGNGGNNGGGGGGGRDHMDRDRGFSRRDDRLSGRNNFNMMSSNDYNNSSNY 211
G G G+ GG G N GG G +D F R G ++ + +
Sbjct: 400 GPVSGGISGGMGSMNSVTGGMGMG-LDRMSSSFDRM-----GPGIGAILERSIDMDRGF 452

Query: 212 NLYGLSASFLESGLISGPLHNKVFVANLDYKVDNKKLKQVFKLAGKVQSVDSLSDKEGNS 271
+ + E +G G N++FV NL + + +KLK+ F G V ++ ++ G S
Sbjct: 453 LSGPMGSGMRERIGSKG---NQIFVRNLPFDLTWQKLKEKFSQCGHVMFAEIKMEN-GKS 508

Query: 272 RGFAVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308
+G + +D P A +A +++ + R + VRLDR
Sbjct: 509 KGCCTVRFDSPEAEKACRIMNGIKISGREIDVRLDR 545

Figure 15B. Multiple Sequence Alignment (ClustalW 1.83)

```

CG9373 Dm -----
KIAA1341 Hs PLSRSEPLSSGGRGGGSGGGMADANKAEVPGATGGDSPHLQPAEPPGEPREPHPAEAEK
MyEF-2 Hs -----
FLJ13071 Hs -----MADANKAEVPGATGGDSPHLQPAEPPGEPREPHPAEAEK

CG9373 Dm ---MSMDASNSVESREKERDRRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNC
KIAA1341 Hs QQPQHSSSSNGVKMENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNRN
MyEF-2 Hs -----MENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNRN
FLJ13071 Hs QQPQHSSSSNGVKMENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNRN

CG9373 Dm RVYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEK
KIAA1341 Hs RVFISNIPYDMKWQAIKDLMREKVGEVTYVELFKDAEGKSRGCGVVEFKDEEFVKKALET
MyEF-2 Hs RVFISNIPYDMKWQAIKDLMREKVGEVTYVELFKDAEGKSRGCGVVEFKDEEFVKKALET
FLJ13071 Hs RVFISNIPYDMKWQAIKDLMREKVGEVTYVELFKDAEGKSRGCGVVEFKDEEFVKKALET

CG9373 Dm MNRYEVNGRELVVKEDHGEQRDQYGRIVRDGGGGGGGGGGVQGGNGGNNGGGGGGGRDHM
KIAA1341 Hs MNKYDLSGRPLNIKEDPDGENARR-----ALQRTGGSFPGGHVPDMGSG-----
MyEF-2 Hs MNKYDLSGRRVNIKEDPDGENARR-----ALQRTGTSFQGSASHSDVSG-----
FLJ13071 Hs MNKYDLSGRPLNIKEDPDGENARR-----ASQRTGGSFPGGHVPDMGSG-----

CG9373 Dm DDRDRGFSRRDDRLSGRNNFNMMSSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFVA
KIAA1341 Hs -----LMNLPPSILNNPNIPPEVISNLQ----AGRLGSTIFVA
MyEF-2 Hs -----LVNLPPSILNNPNIPPEVISNLQ----AGRLGSTIFVA
FLJ13071 Hs -----LMNLPPSILNNPNIPPEVISNLQ----AGRLGSTIFVA

```

CG9373 Dm NLDYKVDNKKLKQVFKLAGKVQSVDSL DKEGNSRGFAVIEYDHPVEAVQAISM LDRQML
KIAA1341 Hs NLDFKVGWKKLKEVF SIA GTVKRADI KEDKD GKS RGM GTVTTFEQ AIEAVQAISM FNQOFL
MyEF-2 Hs NLDFKVGWKKLKEVF SIA GTVKAGSYKEDKD GKS RGM GTVTTFEQ AIEAVQAISM FNQOFL
FLJ13071 Hs NLDFKVGWKKLKEVF SIA GTVKRADI KEDKD GKS RGM GTVTTFEQ AIEAVQAISM FNQOFL

CG9373 Dm FDRRMTVRLDRIPDKNEG I K-----LPEGLGGVGIGLGPNGEPLRDVAHNL PNGGQS
KIAA1341 Hs FDRPMHV KMD DKSVPHEEYRSHD GKT PQLPRGLGGIGMGLGPGGQPISASQLNIG-----
MyEF-2 Hs FDRPMHV KMD DKSVPHEEYRSPD GKT PQLPRGLGGIGMGLGPGGQPISASQLNIG-----
FLJ13071 Hs FDRPMHV KMD DKSVPHEEYRSHD GKT PQLPRGLGGIGMGLGPGGQPISASQLNIG-----

CG9373 Dm QGQLLGNAQQGSQ LGSVGSQPNSSAVSNATTNLLNLTG-VMFGNHAAVQPSVPVAVQKP
KIAA1341 Hs -----GVMGNLG--PGGMGMDGPGFGGMNRIGGGIGFGGLEAMN-----
MyEF-2 Hs -----GVMGNLG--PGGMGMDGPGFGGMNRIGGGIGFGGLEAMN-----
FLJ13071 Hs -----GVMGNLG--PGGMGMDGPGFGGMNRIGGGIGFGGLEAMN-----

CG9373 Dm SLGNNTGSGGLN LNNLNP SILAAVGNLGNQGGNLSNPLLS SSSLN LGLNLGNSGNDNL
KIAA1341 Hs SMGGFGGVG--RMGELYRGAMTSSMERDFGRGDIGINRGFGDSFGRLGSAM-IGGFAGRI
MyEF-2 Hs SMGGFGGVG--RMGELYRGAMTSSMERDFGHRDIGLSRGFGDSFGRLGSAM-IGGITGRI
FLJ13071 Hs SMGGFGGVG--RMGELYRGAMTSSMERDFGRGDIGINRGFGDSFGRLG-----

CG9373 Dm PPSNVGLSN NYSSGGTGGGNSYSSGNNYSGGGSSNLGYNAYSSSGMG GGN GGVGV DGN
KIAA1341 Hs GSSNMGPVGS GISGGMGSMNSVTGGMGMLDRMSSSFDR-----MGP GIGAILERSI
MyEF-2 Hs GSSNMGPVGS GISGGMGSMNSVTGGMGMLDRMSSSFDR-----MGP GIGAILERSI
FLJ13071 Hs -----GGMGMNSVTGGMGMLDRMSSSFDR-----MGP GIGAILERSI

CG9373 Dm DYNTGNPLDVYGGG SNVGN SNVGSANAVGASRSDTII IKNVPITCTWQTLRDKFREIGD
KIAA1341 Hs DMDRG-----FLSGPMGSGMRERIGSKGNQIFVRNL PFDLTWQKLKEKFSQCGH
MyEF-2 Hs DMDRG-----FLSGPMGSGMRERIGSKGNQIFVRNL PFDLTWQKLKEKFSQCGH
FLJ13071 Hs DMDRG-----FLSGPMGSGMRERIGSKGNQIFVRNL PFDLTWQKLKEKFSQCGH

CG9373 Dm VKFAEIRGND-----VGVRFFKERDAELAIALMDGSRLDGRNIKVTYF---
KIAA1341 Hs VMFAEIKMENGKSKGCGTVRFDSPE SAEKACRIMNGIKISGREIDVRLDRNA
MyEF-2 Hs VMFAEIKMENGKSKGCGTVRFDSPE SAEKACRIMNGIKISGREIDVRLDRNA
FLJ13071 Hs VMFAEIKMENGKSKGCGTVRFDSPE SAEKACRIMNGIKISGREIDVRLDRNA

Figure 16. Expression of CG9373 Homologs in Mammalian Tissues

Figure 16A. Real-time PCR analysis of myelin gene expression factor 2 (MEF-2) expression in wild type mouse tissues (DCt Pancreas = 20,90)

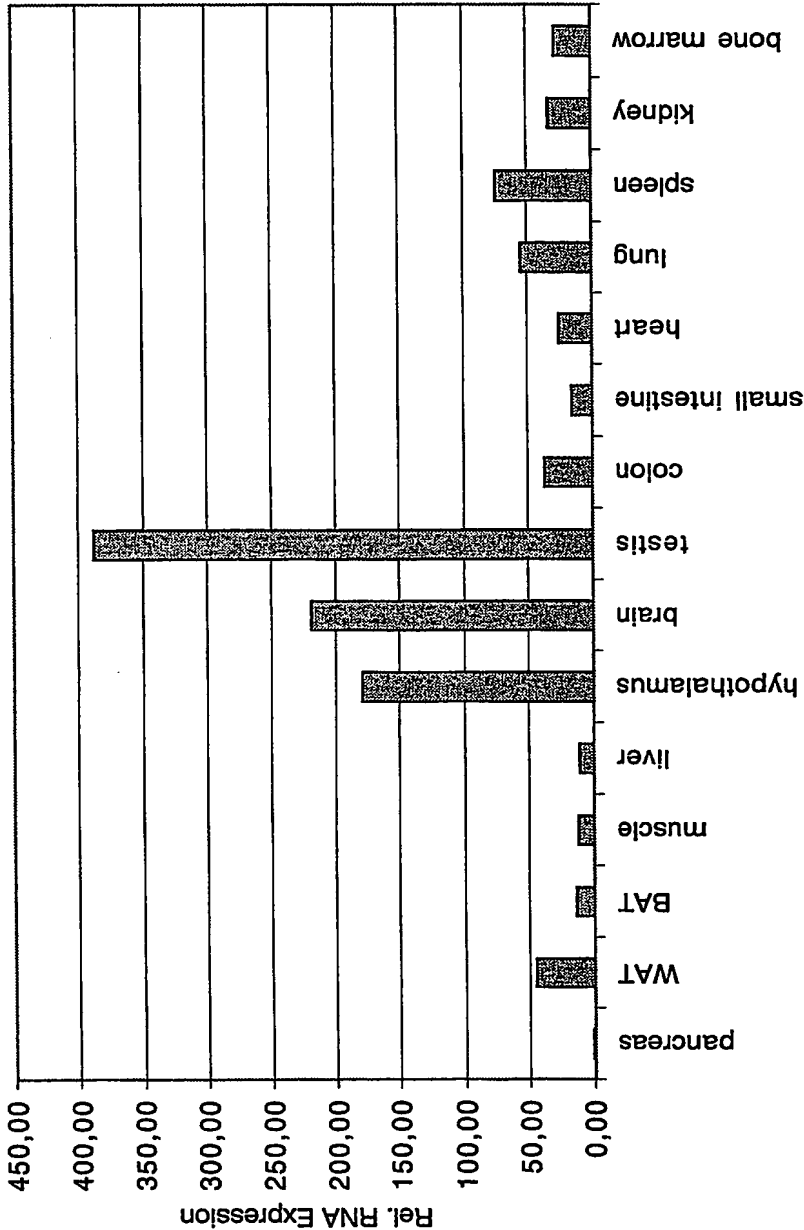


Figure 16B. Real-time PCR analysis of myelin gene expression factor 2 (MEF-2) expression in different mouse models

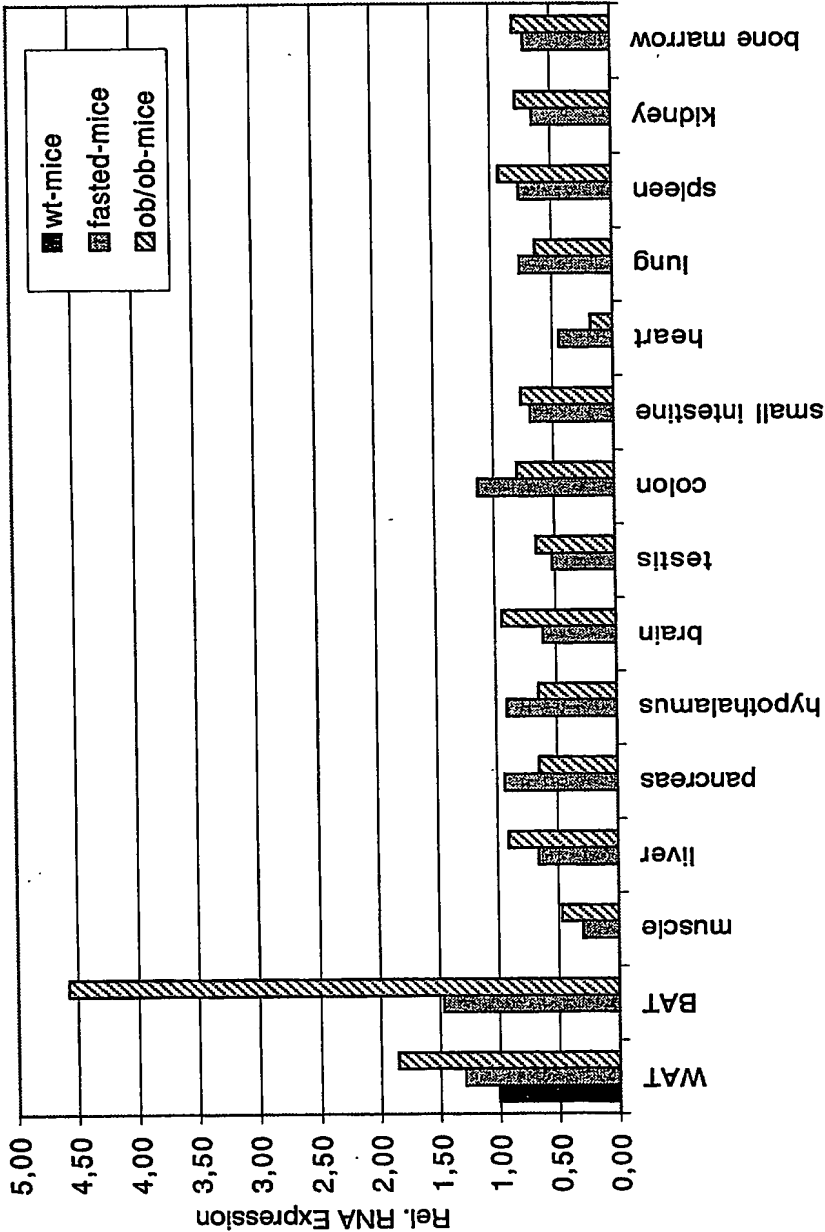


Figure 16C. Real-time PCR analysis of myelin gene expression factor 2 (MEF-2) expression in mice fed with a high fat diet compared to mice fed with a standard diet

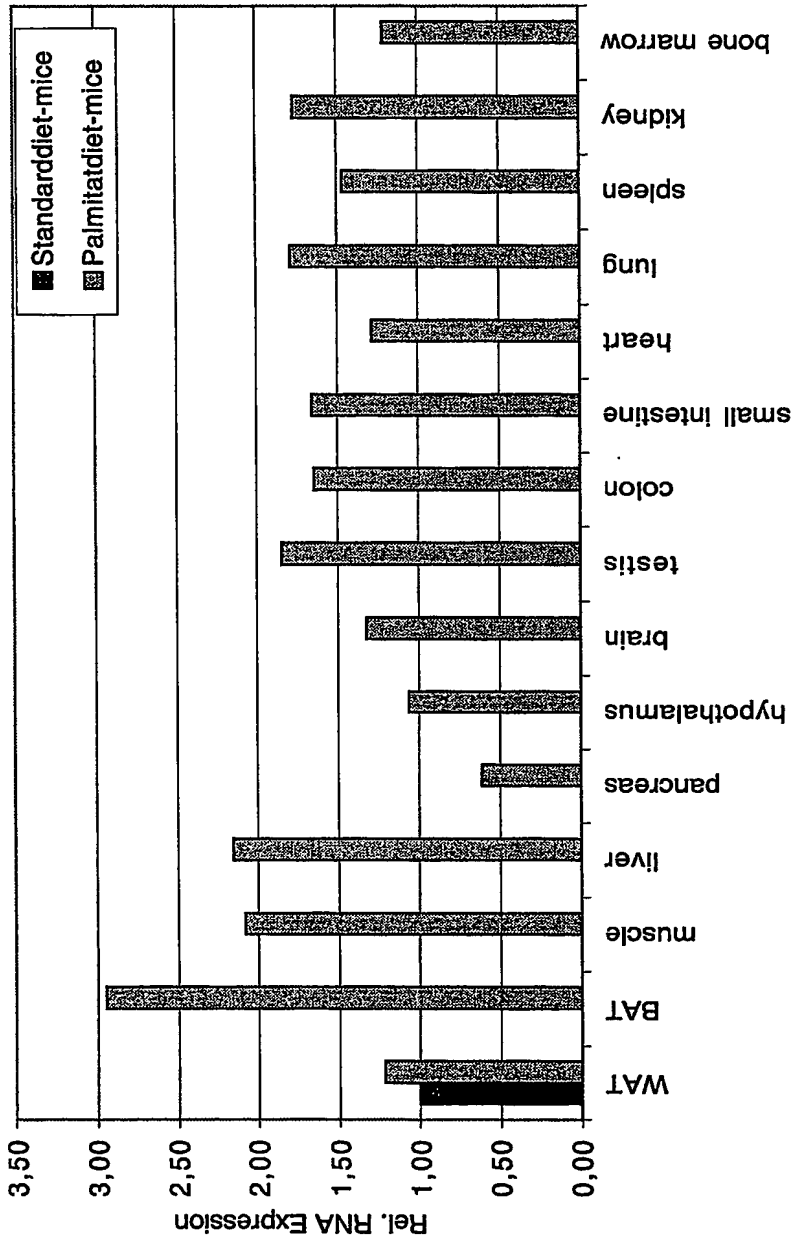


Figure 17. Triglyceride content of a *Drosophila cpo* (GadFly Accession Number CG18434) mutant

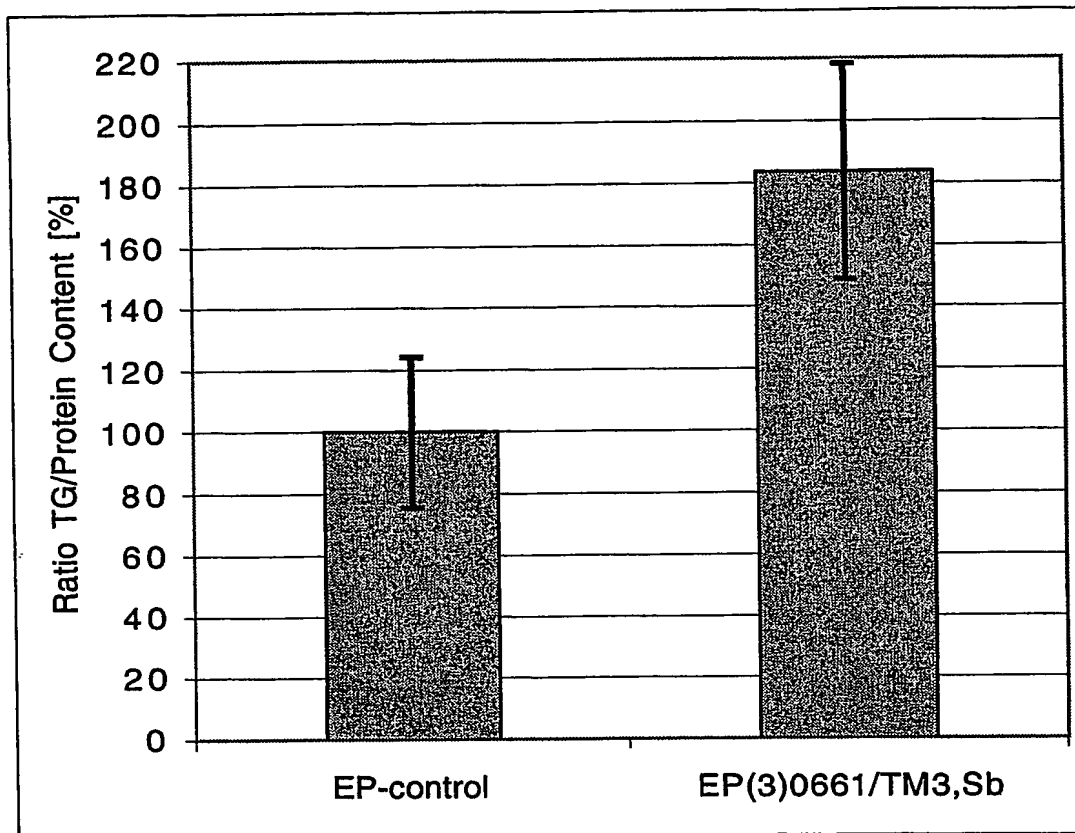


Figure 18. Molecular organisation of the *cpo* gene (GadFly Accession Number CG18434)

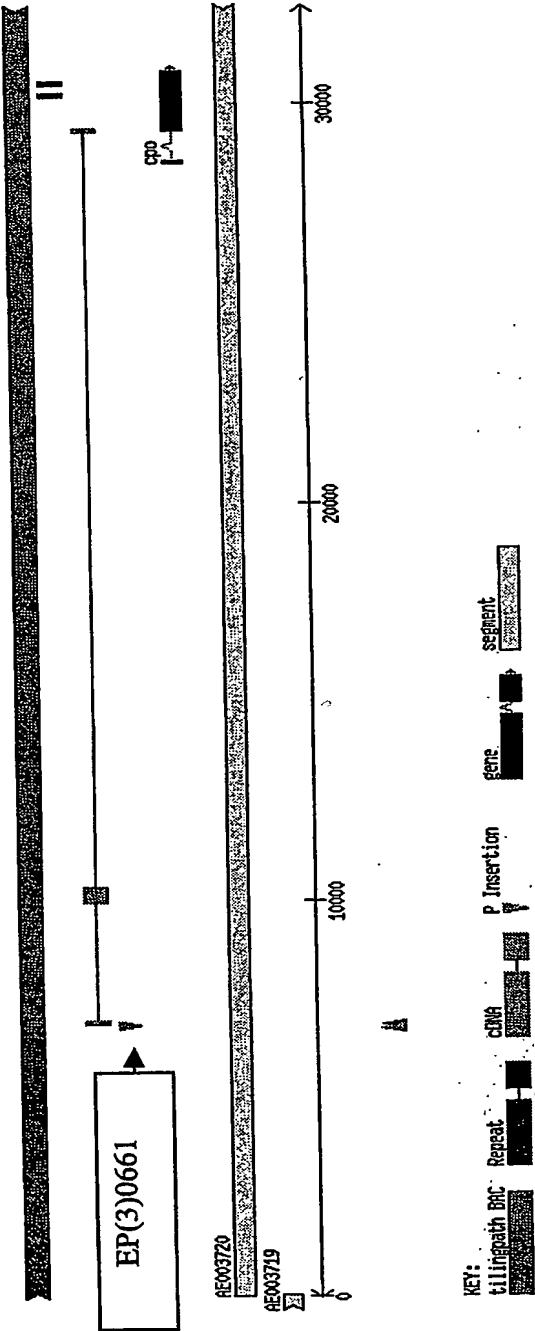


Figure 19. Homology of *Drosophila cpo* (GadFly Accession Number CG31243 and CG18434) to human RNA binding proteins with multiple splicing

Figure 19A. Multiple Sequence Alignment (ClustalW 1.83)

```

cpo Dm      LVKIAN YQDLLGSHHQLLIAATAAAAAAAAAAEPQLQLQHLLPAAPTTPAVISNPINSIGP
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      INQISSSSHPSNNNQAVFEKAITISSIAIKRRPTLPQTPASAPQVLSPSPKRQCAA VVS
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      VLPVTVFPVPFVSVPLFVSVFPVSVKGHPISTHQIAHTHQISHSHPI SHPHHHQLSFA
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      HPTQFAAAVAHHQ000000A00000AV00000AV0000VAYAVAASPOL000000QH
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      RLAQFNQAAAAALLNQHLOQQHQA0000HQA0000SLAHYGGYQLHRYAP0000QHILLSS
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      GSSSSKHNSNNNSNTSAGAASAAVPIATSVAAVPTTGGSLPDSPA HESHSHESNSATASA
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      PTPSPAGSVTSAAPTATATAAAAGSAAATAAATGTPATSAVSDSNNNLN SSSSSNSNSN
NP_006858 Hs -----
IPI00161102 Hs -----MNNGGK

cpo Dm      AIMENQMALAPLGLSQSMDSVNTASNEEEVRTL FVSGLPMDAKPRELYLLFRAYEGYEGS
NP_006858 Hs -----
IPI00161102 Hs -----QEEVRTL FVSGLPLDIKPRELYLLFRPFKGYEGS
-----QVRTLFVSGLPVDIKPRELYLLFRPFK-----

cpo Dm      LLKVTSKNGKTASPVGFVTFHTRAGAEAAKQDLQGVRFDPDMPQTIRLEFAKSNTKVS KP
NP_006858 Hs -----
IPI00161102 Hs -----PVGFVSFDSRSEAEAAKNALNGIRFDPEIPQTLRLEFAKANTKMAKN
-----PVGFVTFDSRAGAEAAKNALNGIRFDPENPQTLRLEFAKANTKMAKS

cpo Dm      KPQPNTATTASHPALMHPLTG-----HLGGPFFPGGP ELWHHPLAYSAAAAAELPG-----
NP_006858 Hs -----
IPI00161102 Hs -----KLVGTPNPSTPLPNTVPQFIAREPYELTVPALYPSSPEVWAPYPLYPAELAPALPPP AFT
-----KLMATPNPSNVHPALGAHFIA RDPYDLMGAALIPASPEAWAPYPLYTTTELTPAISHAAFT

cpo Dm      -----AAALQHATLVHPALHPQVP---VRSYL
NP_006858 Hs -----
IPI00161102 Hs -----YP-----ASLHAQMRWLPPSEATSQGWKSRQFC
-----YPTATAAAAAALHAQVRWYPSSD TTQQGWKYRQFC

```

FIGURE 19B. Amino acid sequence encoded by Drosophila gene CG31243 (GadFly Accession Number), SEQ ID NO:1

>CG31243-PA (AE003720) [gene_syn=CG31243] [prot_desc=CG31243 gene product from transcript CG31243-RA]

```
1  LVKIANQDL  LGSHHQLLIA  ATAAAAAAAA  AEPQLQLQHL  LPAAPTTPAV  ISNPINSIGP
61  INQISSSSHP  SNNNQQAVFE  KAITISSIAI  KRRPTLPQTP  ASAPQVLSPS  PKRQCAAAYS
121 VLPVTVFPV  PVSVPPLPVS  PVPVSVKGHP  ISHTHQIAHT  HQISHSHPI  HPHHHQLSFA
181 HPTQFAA  AAVA  AHHQ  QQQQQQ  AQQQQQAVQQ  QQQQAVQQQQ  VAYAVAASPQ  LQQQQQQQQH
241 RLAQFNQAAA  AALLNQHLQQ  QHQ  AQQQQQH  AQQQSLAHYG  GYQLHRYAPQ  QQQQHILLSS
301 GSSSSKHNSN  NNSNTSAGAA  SAAVPIATSV  AAVPTTGGSL  PDSPAHEHS  HESNSATASA
361 PTTSPAGSV  TSAAPTATAT  AAAAGSAAAT  AAATGTPATS  AVSDSNNNLN  SSSSSNSNSN
421 AIMENQMALA  PLGLSQSMDS  VNTASNEEEV  RTLFSVGLPM  DAKPRELYLL  FRAYEGYEGS
481 LLKVTSKNGK  TASPVGFTF  HTRAGAEAAK  QDLQGVRFDP  DMPQTIRLEF  AKSNTKVS  KP
541 KPQNTATTA  SHPALMHPLT  GHLGGPFFPG  GP  ELWHHPLA  YSAAAAELP  GAAALQHATL
601 VHPALHPQVP  VRSYL
```

Figure 20. Expression of a human *cpo* homolog in mammalian (human) tissue
Quantitative analysis of RNA binding protein with multiple splicing (RBPMS) expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

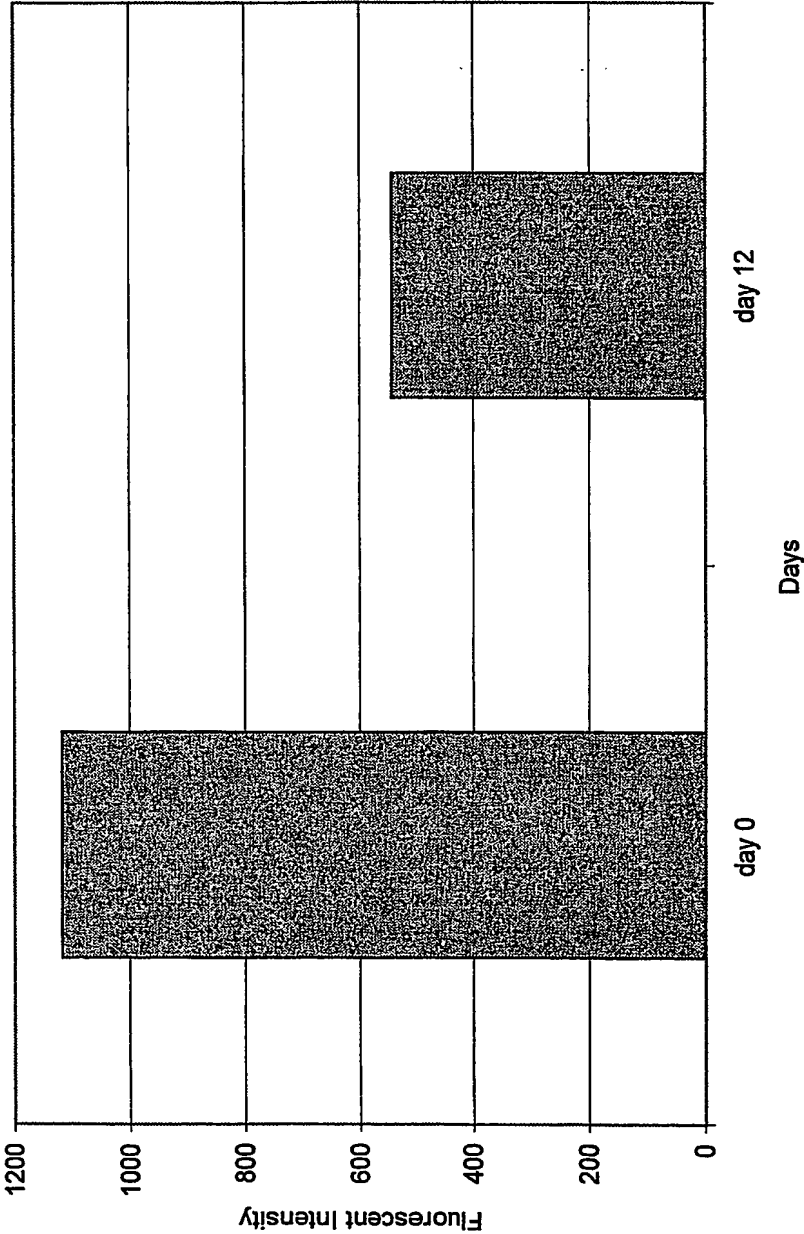


Figure 21. Triglyceride content of a *Drosophila Jafrac1* (GadFly Accession Number CG1633) mutant

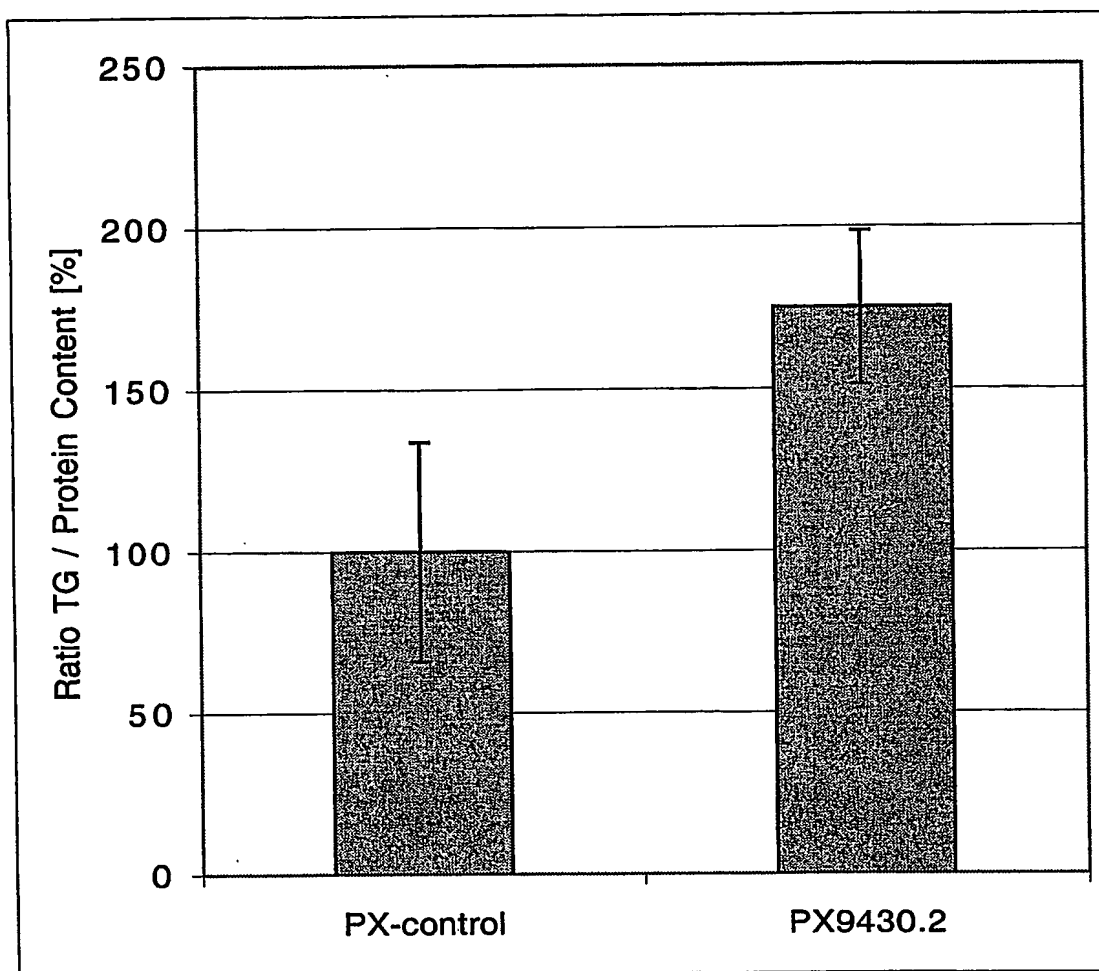


Figure 22. Molecular organisation of the *Jafrac1* gene (GadFly Accession Number CG1633)

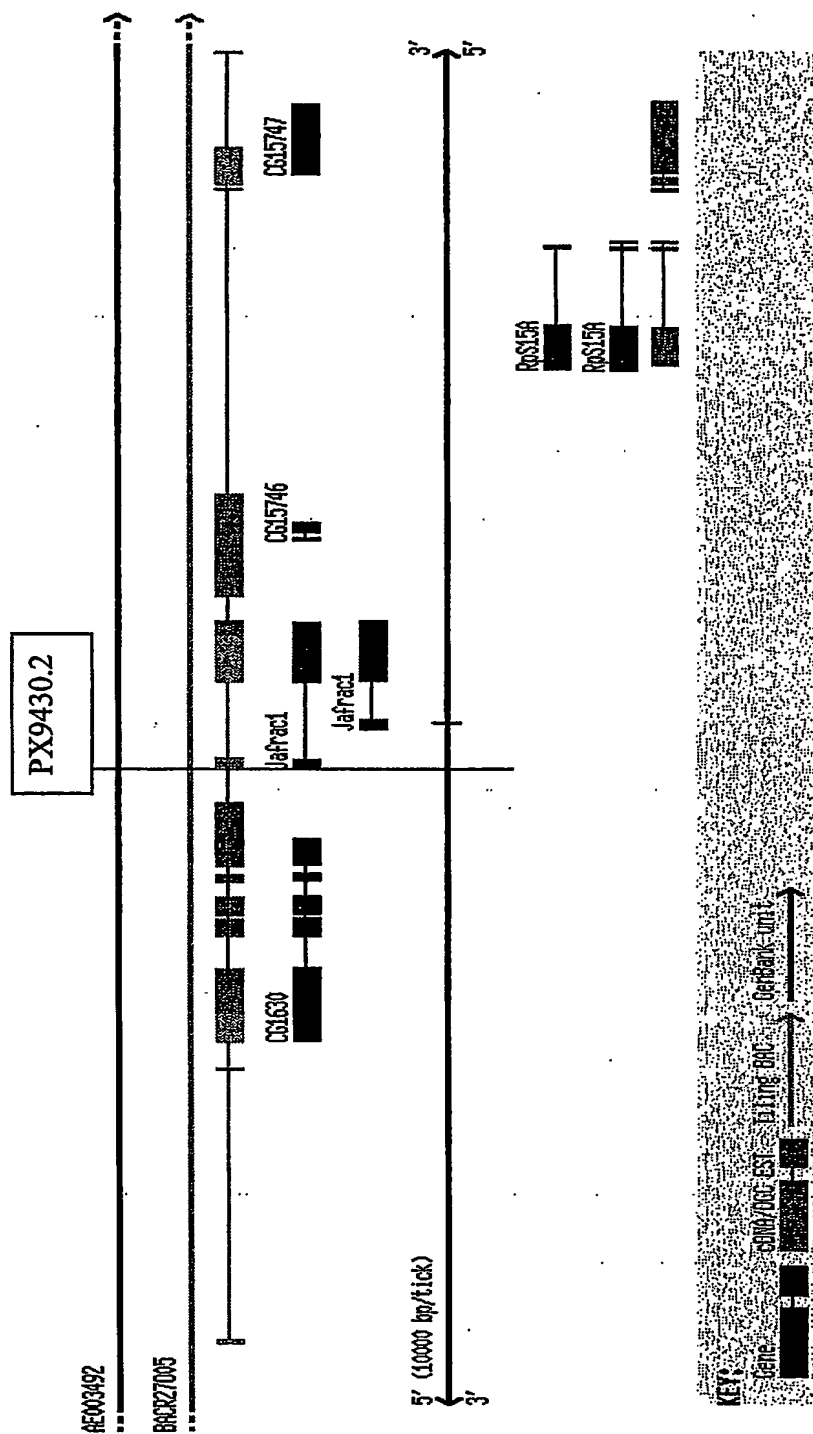


Figure 23. Homology of *Drosophila Jafrac1* (GadFly Accession Number CG1633) to human peroxiredoxin 1 and human peroxiredoxin 2 (similar to peroxiredoxin 1)

Figure 23A. BLASTP results for *Jafrac1*

Homology to human protein XP_009063.2 (GenBank Accession Number)

ref|XP_009063.2| (XM_009063) peroxiredoxin 2 [Homo sapiens]
Length = 198

Score = 283 bits (723), Expect = 9e-76
Identities = 134/188 (71%), Positives = 157/188 (83%)

```
Query: 3   QLQKPAPAFAGTAVVNGVFKDIKLSDYKGKYLVLFFYPLDFTFVCPTETIIAFSESAAEFR 62
          ++ KPAP F  TAVV+G FK++KLSDYKGKY+VLFFYPLDFTFVCPTETIIAFS  A +FR
Sbjct: 7   RIGKPAPDFKATAVVDGAFKEVKLSDYKGKYVVLFFYPLDFTFVCPTETIIAFSNRAEDFR 66

Query: 63  KINCEVIGCSTDSQFTHLAWINTPRKQGGLGSMIDIPLLADKSMKVARDYGVLDDEETGIPF 122
          K+ CEV+G S DSQFTHLAWINTPRK+GGLG ++IPLLAD + +++ DYGV L  + GI +
Sbjct: 67  KLGCEVLGVSVDSQFTHLAWINTPRKEGGLGPLNIPLLADVTRRLSEDYGV LKTDEGIAY 126

Query: 123 RGLFIIDDKQNL RQITVNDLPVGRSVEETLRLVQAFQYTDKYGEVCPANWKPGQKTMVAD 182
          RGLFIID K  LRQITVNDLPVGRSV+E LRLVQAFQYTD++GEVCPA WKPG  T+  +
Sbjct: 127 RGLFIIDGKGVLRQITVNDLPVGRSVDEALRLVQAFQYTDHGEVCPAGWKPGSDTIKPN 186

Query: 183 PTKSKEYF 190
          SKEYF
Sbjct: 187 VDDSKEYF 194
```

Homology to human protein NP_002565.1 (GenBank Accession Number)

ref|NP_002565.1| (NM_002574) peroxiredoxin 1; Proliferation-associated gene A;
proliferation-associated gene A (natural killer-enhancing factor A) [Homo sapiens]
ref|XP_001393.2| (XM_001393) peroxiredoxin 1 [Homo sapiens]
Length = 199

Score = 281 bits (718), Expect = 3e-75
Identities = 135/185 (72%), Positives = 154/185 (82%), Gaps = 1/185 (0%)

```
Query: 7   PAPAFAGTAVV-NGVFKDIKLSDYKGKYLVLFFYPLDFTFVCPTETIIAFSESAAEFRKIN 65
          PAP F  TAV+ +G FKDI LSDYKGKY+V FFYPLDFTFVCPTETIIAFS+ A EF+K+N
Sbjct: 11  PAPNFKATAVMPDGQFKDISLSDYKGKYVVFVFFYPLDFTFVCPTETIIAFSDRAEEFKKLN 70

Query: 66  CEVIGCSTDSQFTHLAWINTPRKQGGLGSMIDIPLLADKSMKVARDYGVLDDEETGIPFRGL 125
          C+VIG S DS F HLAW+NTP+KQGGLG M+IPL++D  +A+DYGV L  + GI FRGL
Sbjct: 71  CQVIGASVDSHFCHLAWVNTPKKQGGLGPMNIPLVSDPKRTIAQDYGV LKADEGISFRGL 130

Query: 126 FIIDDKQNL RQITVNDLPVGRSVEETLRLVQAFQYTDKYGEVCPANWKPGQKTMVADPTK 185
          FIIDDK LRQITVNDLPVGRSV+ETLRLVQAFQ+TDK+GEVCPA WKPG  T+  D K
Sbjct: 131 FIIDDKGILRQITVNDLPVGRSVDETLRLVQAFQFTDKHGEVCPAGWKPGSDTIKPDVQK 190

Query: 186 SKEYF 190
          SKEYF
Sbjct: 191 SKEYF 195
```

Figure 23B. Multiple Sequence Alignment (ClustalW 1.83)

```
Jafrac1 Dm MP----QLQKPAPAFAGTAVV-NGVFKDIKLSDYKGKYLVLFFYPLDFTFVCPTETIIAFS
PRDX1 Hs  MSSGNAKIGHAPNFKATAVMPDGQFKDISLSDYKGKYVVFYPLDFTFVCPTETIIAFS
PRDX2 Hs  MASGNARIGKPAPDFKATAVV-DGAFKEVKLSDYKGKYVVLFFYPLDFTFVCPTETIIAFS

Jafrac1 Dm ESAAEFRKINCEVIGCSTDSQFTHLAWINTPRKQGGLGSMDIPLLADKSMKVARDYGVL
PRDX1 Hs  DRAEEFKKLNCQVIGASVDSHFCHLAWVNTPKKQGGLGPMNIPLVSDPKRTIAQDYGVLK
PRDX2 Hs  NRAEDFRKLGCEVLGVSVD SQFTHLAWINTPRKEGGLGPLNIPLLADVTRRLSEYGVK

Jafrac1 Dm EETGIPFRGLFIIDDKQNL RQITVNDLPVGRSVEETLRLVQAFQYTDKYGEVCPANWKPG
PRDX1 Hs  ADEGISFRGLFIIDDKGIL RQITVNDLPVGRSVDETLRLVQAFQYTDKHGEVCPAGWKPG
PRDX2 Hs  TDEGIAYRGLFIIDGKGVLRQITVNDLPVGRSVDEALRLVQAFQYTDEHGEVCPAGWKPG

Jafrac1 Dm QKTMVADPTKSKEYFETTS
PRDX1 Hs  SDTIKPDVQKSKEYFSKQK
PRDX2 Hs  SDTIKPNVDDSKEYFSKHN
```

Figure 24. Expression of a human *Jaftrac1* homolog in mammalian (human) tissue
Quantitative analysis of Peroxiredoxin 1 (PRDX1) expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

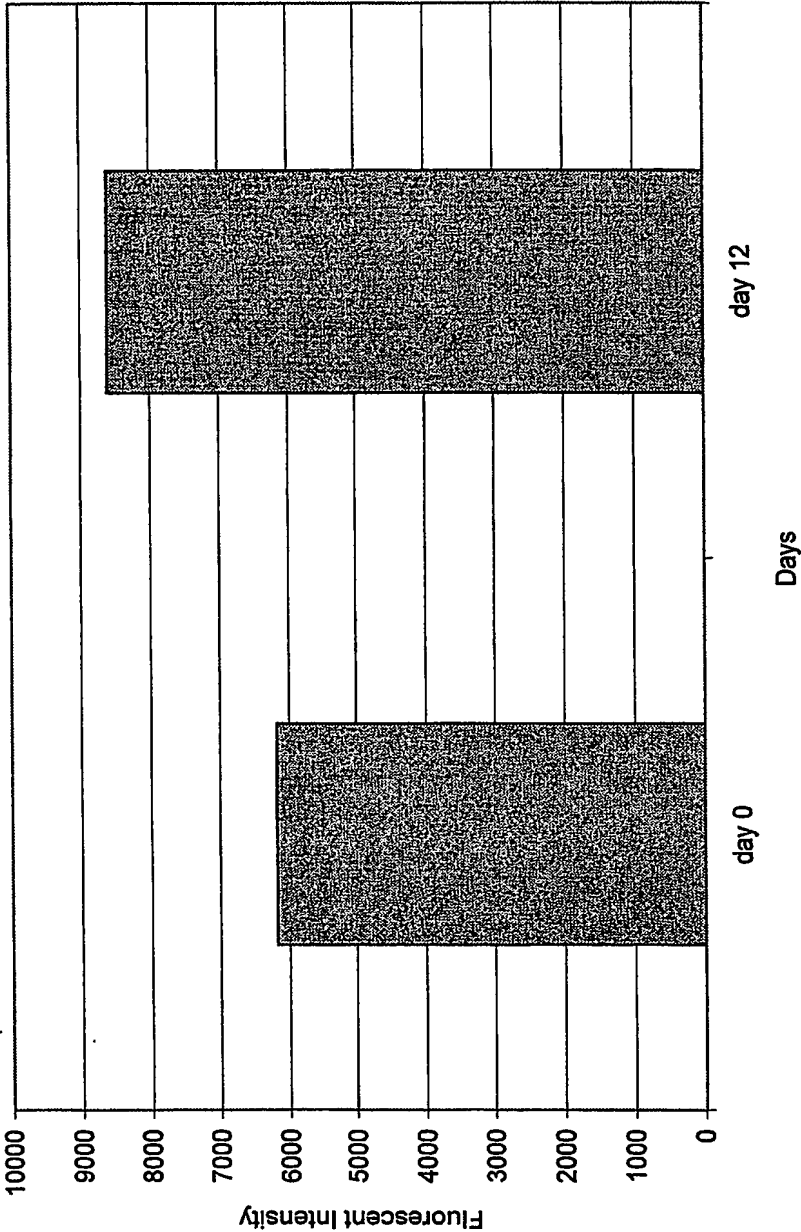


Figure 25. Triglyceride content of a *Drosophila* CG14440 (GadFly Accession Number) mutant

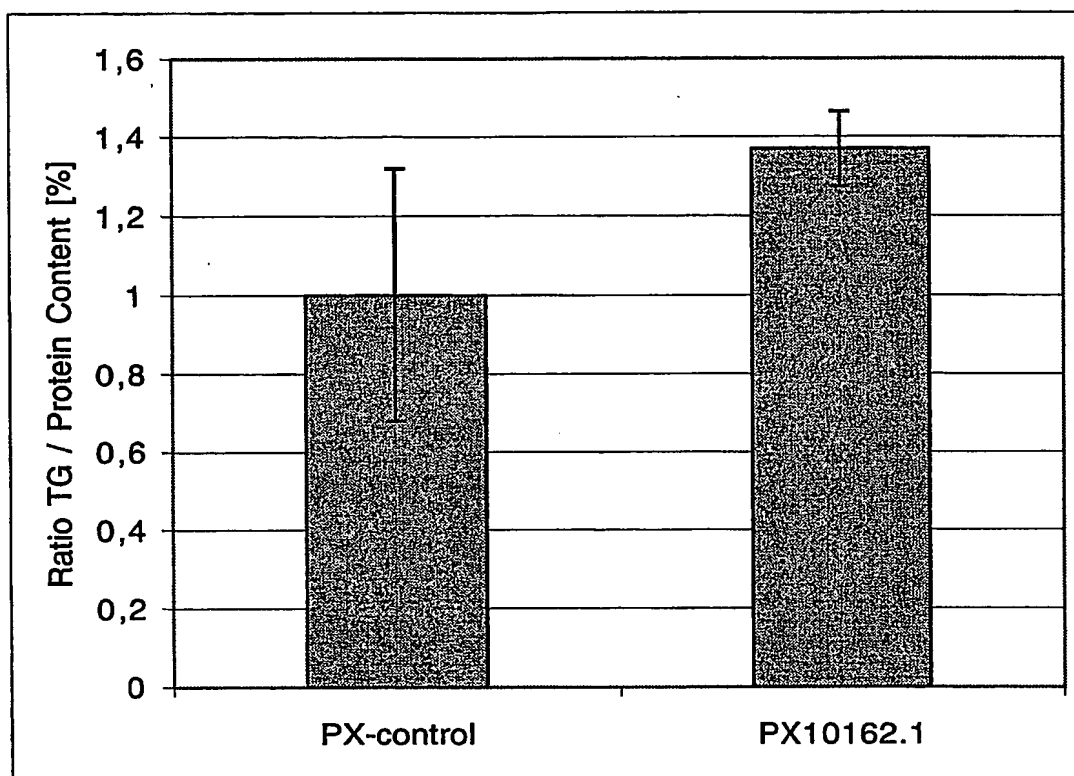


Figure 26. Molecular organization of the CG14440 gene (GadFly Accession Number)

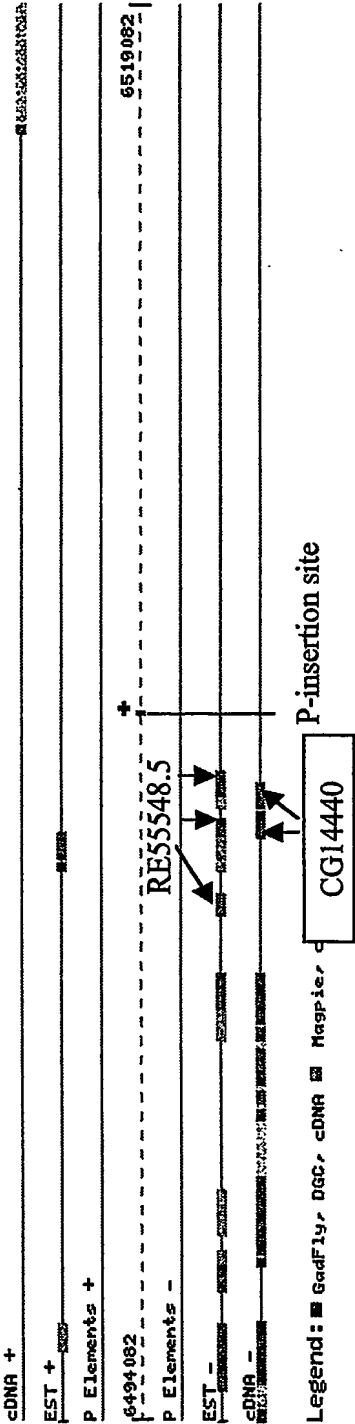


Figure 27. BLASTP results for CG14440 (GadFly Accession Number)**Homology to human protein NP_060000.1 (GenBank Accession Number)**

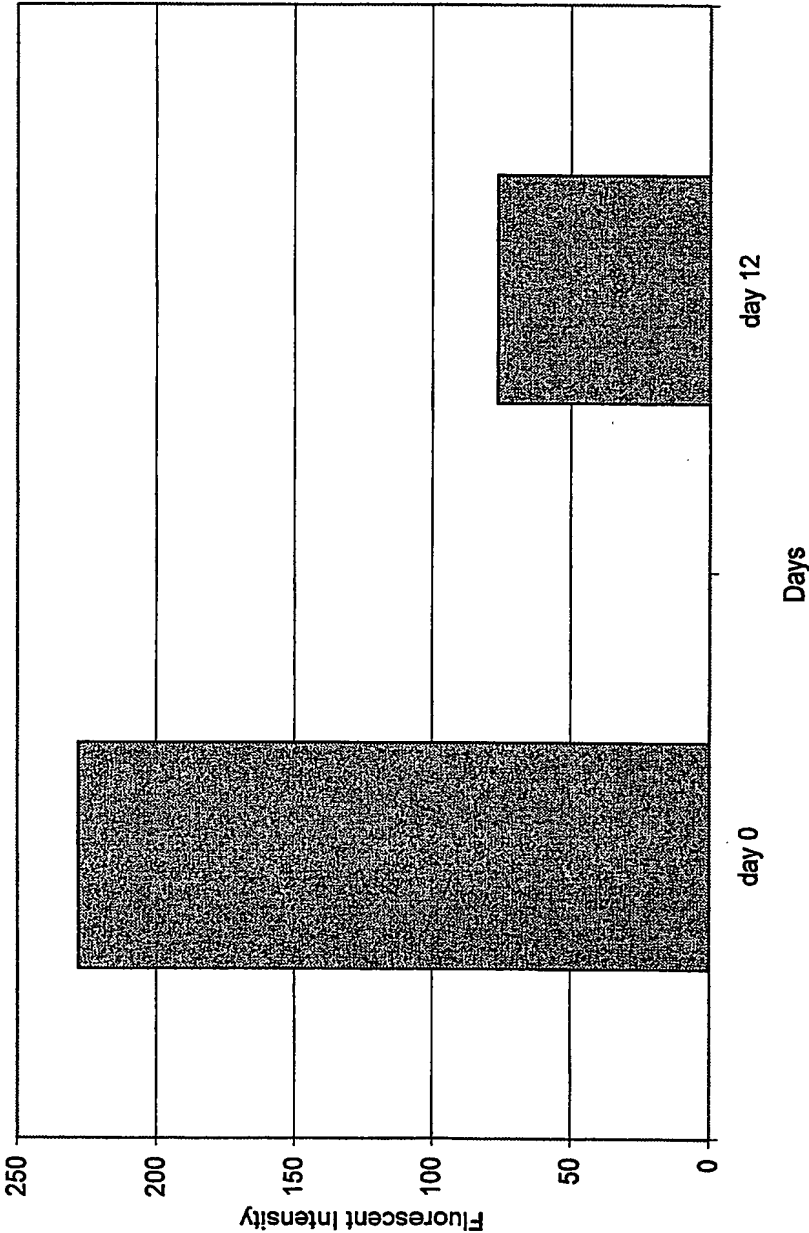
ref|NP_060000.1| (NM_017530) hypothetical protein LOC55565 [Homo sapiens]
Length = 370

Score = 77.4 bits (189), Expect = 2e-13
Identities = 41/106 (38%), Positives = 62/106 (57%)

Query: 195 QGQSSRAQKAARRRSNESIEARERRLERNAARMRDKRAKESAEYRVRLAKNAEANRVRR 254
+ Q+ +K A RR NE +E R +RLER + +R E+ E VR ++ EA R++R
Sbjct: 207 EAQTPSVRKWALRRQNEPLEVRLQRLERERTAKKSRRDNETPEEREVRRMRDREAKRLQR 266

Query: 255 QNETEVQRTLRMLMKNAARQRLRRASETVEERKKRLAKAAERMRIAR 300
ET+ QR RL ++ RL+RA+ET E+R+ RL + E R+ R
Sbjct: 267 MQETDEQRARRLQDRREAMRLKRANETPEKRQARLIREREAKRLKR 312

Figure 28. Expression of the human CG14440 homolog in mammalian (human) tissue
Quantitative analysis of human hypothetical protein LOC55565 expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes



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(54) Title: **PROTEINS INVOLVED IN THE REGULATION OF ENERGY HOMEOSTASIS**

(57) Abstract: The present invention discloses novel uses for energy homeostasis regulating proteins and polynucleotides encoding these in the diagnosis, study, prevention, and treatment of metabolic diseases and disorders.

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INTERNATIONAL SEARCH REPORT

International Application No

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A. CLASSIFICATION OF SUBJECT MATTER
 IPC 7 A61K38/17 A61K48/00 C12Q1/68 A01K67/027 C12N5/10
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B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
 IPC 7 A61K

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Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, EMBASE, CHEM ABS Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 97/02048 A (MILLENNIUM PHARM INC) 23 January 1997 (1997-01-23) claims 1,12,17,22	1-15, 18-29,31
Y	WO 97/19952 A (TARTAGLIA LOUIS A ;WHITE DAVID W (US); TEPPER ROBERT I (US); CULPE) 5 June 1997 (1997-06-05) abstract; claims 14,27,28,37,38,50,62	1-15, 18-29,31
Y	FLEURY C ET AL: "UNCOUPLING PROTEIN-2: A NOVEL GENE LINKED TO OBESITY AND HYPERINSULINEMIA" NATURE GENETICS, NEW YORK, NY, US, vol. 15, no. 3, 1 March 1997 (1997-03-01), pages 269-272, XP002064499 ISSN: 1061-4036 abstract page 271, column 2	1-15, 18-29,31
	----- -/-	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

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Date of mailing of the international search report

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Gonzalez Ramon, N

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 03/04650

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>FORTINI M. E. ET AL: "A survey of human disease gene counterparts in the drosophila genome" J CELL BIOL, vol. 150, no. 2, 24 July 2000 (2000-07-24), pages f23-f29, XP002257035 abstract; table 1 page F26, paragraph 3 page F29, paragraph 3 -----</p>	<p>1-15, 18-29,31</p>
A	<p>CHIESI M ET AL: "PHAMACOTHERAPY OF OBESITY: TARGETS AND PERSPECTIVES" TRENDS IN PHARMACOLOGICAL SCIENCES, ELSEVIER TRENDS JOURNAL, CAMBRIDGE, GB, vol. 22, no. 5, May 2001 (2001-05), pages 247-254, XP001080052 ISSN: 0165-6147 page 251, column 2; table 1 -----</p>	<p>1-15, 18-29,31</p>
A	<p>"CG7956" FLYBASE.BIO.INDIANA.EDU, [Online] page 1, XP002256412 Retrieved from the Internet: URL:http://flybase.bio.indiana.edu/.bin/fb idq.html?FBgn0038890&resultlist=fbgn9869.d ata[0]> [retrieved on 2003-10-02] abstract -----</p>	<p>1-15, 18-29,31</p>

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP 03/04650

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 16, 17, 30
because they relate to subject matter not required to be searched by this Authority, namely:
Although claim 20 is directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☒ Claims Nos.: partially 1-31
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-31 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box 1.1

Although claim 20 is directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Continuation of Box 1.1

Claims Nos.: 16, 17, 30

Rule 39.1(ii) PCT - Animal variety
Rule 39.1(ii) PCT - Essentially biological process for the production of animals

Continuation of Box 1.2

Claims Nos.: partially 1-31

Present claims 1-31 relate to compounds defined by reference to desirable characteristics or properties, namely: "functional fragment" (claims 1, 2, 14, 15, 20-22, 30, 31); "effector/modulator" (claims 1, 14, 15, 31); "a variant" (claim 2); "a binding target" (claims 21); "a candidate agent" (claims 21, 22).

The claims cover all compounds having these characteristics or properties, whereas the application provides neither support within the meaning of Article 6 PCT nor disclosure within the meaning of Article 5 PCT for such compounds. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the compound by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible. Consequently, the search for the first invention has been carried out for those parts of the claims which appear to be clear, supported and disclosed, namely those parts relating to the compounds explicitly disclosed in the examples in relation to CG7956 nucleic acid or polypeptide encoded thereby.

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Chapter II procedure. If the application proceeds into the regional phase before the EPO, the applicant is reminded that a search may be carried out during examination before the EPO (see EPO Guideline C-VI, 8.5), should the problems which led to the Article 17(2) declaration be overcome.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: partially 1-31

Pharmaceutical composition comprising a CG7656 nucleic acid molecule or a polypeptide encoded thereby. Use of the same for the treatment of obesity, diabetes and/or metabolic syndrome. Methods of screening using the same.

2. claims: partially 1-31

Pharmaceutical composition comprising an aralar 1 nucleic acid molecule or a polypeptide encoded thereby. Use of the same for the treatment of obesity, diabetes and/or metabolic syndrome. Methods of screening using the same.

3. claims: partially 1-31

Pharmaceutical composition comprising a how nucleic acid molecule or a polypeptide encoded thereby. Use of the same for the treatment of obesity, diabetes and/or metabolic syndrome. Methods of screening using the same.

4. claims: partially 1-31

Pharmaceutical composition comprising a CG9373 nucleic acid molecule or a polypeptide encoded thereby. Use of the same for the treatment of obesity, diabetes and/or metabolic syndrome. Methods of screening using the same.

5. claims: partially 1-31

Pharmaceutical composition comprising a cpo nucleic acid molecule or a polypeptide encoded thereby. Use of the same for the treatment of obesity, diabetes and/or metabolic syndrome. Methods of screening using the same.

6. claims: partially 1-31

Pharmaceutical composition comprising a Jafrac 1 nucleic acid molecule or a polypeptide encoded thereby. Use of the same for the treatment of obesity, diabetes and/or metabolic syndrome. Methods of screening using the same.

7. claims: partially 1-31

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Pharmaceutical composition comprising a CG14440 nucleic acid molecule or a polypeptide encoded thereby. Use of the same for the treatment of obesity, diabetes and/or metabolic syndrome. Methods of screening using the same.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 03/04650

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